



SEQUENCE LISTING

<110> Egan, Sean E.
Wang, Wei
Sengar, Ameet

<120> ESE GENES AND PROTEINS

<130> 3477-89

<140> US 09/674,237
<141> 2001-07-24

<150> PCT/CA99/00375
<151> 1999-04-27

<150> US 60/118,739
<151> 1999-02-05

<150> CA 2230201
<151> 1998-04-27

<160> 37

<170> PatentIn version 3.3

<210> 1
<211> 5084
<212> DNA
<213> Mus musculus

<400> 1
cggcacgagg aggagtggag cggcgcgaaa gggcgcgacag cttgggttgc tccgtatcg 60
gcggctcgca agggagcatc ccgagcgggc tccgggacgg ccgggaggca ggcaggcgaa 120
cgggcgaaaa tggtgtgcgc ggctgcggac tcggcggtcc tcgcgcggcg tgccggctgc 180
actgatttgt gtgagggcg gccgcgcga cccgcggaa gatgaggcg tgcgtatgtc 240
ggtaacgta atagaaccat ggctcagttt cccacaccc tcgggtgttag cctggatgtc 300
tggccataa ctgtggagga aaggccaag catgaccagc agttcccttag cctgaagccg 360
atagcggat ttattactgg tgatcaagcg aggaactttt tttccaaatc tgggttacct 420
cagcctgtct tagcacaaat atggcgcta gcggacatga ataacgtatgg aaggatggat 480
caagtggaaat ttccatagc catgaagctt atcaaactga agctacaagg atatcagctc 540
ccctccacac ttccccctgt catgaaacag caaccagttt ctatccatcg tgcaccagca 600
tttggatag gagggattgc tagcatgcca ccactcacag ctgttgcgtcc tggccatgt 660
ggctccattc cagttgttgg aatgtctcca cccttagtat ctctgtccc tccagcagca 720
gtgcctcccc tggctaacgg ggctcctccc gtcatacagc ctctgcgtgc gtttgcgcata 780
cctgcagcca catggccaaa gagttcttcc ttcagcagat ctggtccagg gtcacaattt 840
aacactaagt tacagaaggc acaatcatcc gatgtcgcca ggcggccctcc agcagcagaa 900

tgggctgtgc ctcagtcatac aaggctgaaa tacagggcagt tattcaacag ccacgacaaa	960
actatgagtg gacacttaac aggtccccag gcaagaacta ttctcatgca atcaagttt	1020
ccccaggctc agctggcttc aatatggaat ctttctgaca ttgatcaaga tggaaaactc	1080
actgcagaag aatttatcct agctatgcac ctaattgatg ttgccatgtc tggcagcca	1140
ctgccgccc tcctgcctcc agaatacatc cctccttct tcagaagagt tggctccggc	1200
agtggatgt cogtcataag ctcttcttct gtggatcaga ggctgcctga ggagccgtcg	1260
tcagaggatg agcagcagcc agagaagaaa ctgcctgtga catttgaaga taagaagcgg	1320
gagaacttcg agcgaggcag tgtggagctg gagaagcgcc gccaagcgct cttggagcag	1380
cagcgcaaag agcaggagcg gttggcttag ctggagcgcg ccgagcagga gagaaagag	1440
cgggagcgcc aggagcagga gccaagcgag cagctggagc tggagaagca gctggagaag	1500
cagcgggagc tggagcggca gcgagaggag gagaggagga aggagatcga gagcgcgag	1560
gccgcaaaac gggacttggaa aaggcagcga caacttgaat gggAACGGAA ccggagacag	1620
gaactcctga atcagaggaa caaggagcag gagggcaccg tggcctgaa ggcaaggagg	1680
aagactctgg agttttagtt agaagctctg aatgacaaaa agcatcagct agaaggaaaa	1740
ttcaggata tcaggtgtcg actggcaacc cagaggcaag aaattgagag cacgaacaag	1800
tctagagagc taagaattgc tgaaatcacc cacttacagc agcagttgca ggaatctcag	1860
caaattgttg gaagacttat tccagagaaa cagatactca gtgaccagtt aaaacaagtc	1920
cagcagaaca gtttgcatac agactcgctt cttaccctca aaagagcctt ggaagcaaag	1980
gagctggccc ggcagcagct ccgggagcag ctggacgagg tggagagaga gaccaggtca	2040
aagctgcagg agattgtatgt tttcaacaac cagctgaagg aactgagaga gatacatagc	2100
aaacagcaac tccagaagca gaggtccctg gaggcagcgc gactgaagca gaaagagcag	2160
gagaggaaga gcctggagtt agagaagcaa aaggaagacg ctcagagacg agttcagggaa	2220
agggacaagc aatggcttggaa gcatgtgcag caggaggagc agccacgccc ccggaaaccc	2280
cacgaggagg acagactgaa gagggaaagac agtgcagga agaaggaggc ggaagagaga	2340
gccaaggccgg aaatgcaaga caagcagagt cggctttcc atccgcataa ggagccagct	2400
aagctggcca cccaggcacc ctggcttacc acagagaaaag gcccgcattac catttctgca	2460
caggagatgt taaaagtggatattaccga ggcgtgtacc cctttgaatc cagaagtcac	2520
gatgagatca ccatccagcc aggatata gtcatggtgg atgaaagcca gactggagag	2580
ccaggatggc ttggaggaga gctgaaaggg aagacggat ggtccctgc aaactatgca	2640
gaaaagattc cagaaaatga ggttcccact ccagccaaac cagtgaccga tctgacatct	2700

gcccctgccc ccaaactggc tctgcgtgag acccctgctc ctttgcctgt gacctttct	2760
gagccctcca caaccccaa caactggca gacttcagtt ccacgtggcc cagcagctca	2820
aacgagaagc cagaaacgga caactggat acgtggcggt ctcagccttc tctgaccgta	2880
cctagtgctg gccagttacg gcagagatca gccttaccc cagccacago cactggctcc	2940
tccccatctc ccgtcctggg ccagggtgaa aaggtggaag ggctacaagc gcaagccctg	3000
tatccctgga gagccaaaaa agacaaccac taaaattta acaaaagtga cgtcatcacc	3060
gttctggaac agcaagacat gtgggggtt ggagaagttc aaggtcagaa gggttgggtc	3120
cccaagtctt acgtgaaact catttcaggg cccgtaagga aatccacaag catcgatact	3180
ggccctactg aaagtctgc tagtctaaag agagtggctt cccggccgc caagccagcc	3240
attccoggag aagagttat tgccatgtac acatacgaga gttctgagca aggagattta	3300
acctttcagc aaggggatgt gattgtggtt accaagaaaag atggtaactg gtggacggga	3360
acggtggcg acaagtccgg agtctccct tctaactatg tgaggcttaa agattcagag	3420
ggctctggaa ctgctggaa aacagggagt ttagaaaaa aacctgaaat tgcccaggtt	3480
attgcttcct acgctgctac tggtcccgaa caactcaccc tggctcctgg gcagctgatt	3540
ctgatccgga aaaagaaccc aggtggatgg tgggaaggag aactgcaago tcgagggaaa	3600
aagcgccaga tagggtggtt tccagcaaat tatgtcaaac ttctaagccc cggaacaagc	3660
aaaatcaccc caactgagct acccaagacc gcagtgcagc cagcagtgtg ccaggtgatc	3720
gggatgtacg attacaccgc ccagaacgat gacgaactag cttcagcaa aggccagatc	3780
atcaacgtcc tcaacaagga ggaccggac tggggaaag gagaagtcag tggcaagtt	3840
gggctttcc catccaatta tgtaaagctg accacagaca tggacccag ccagcaatga	3900
atcatatgtt gtccatcccc ccctcaggct tgaaagtccct caaagagacc cactatccca	3960
tatcactgcc cagagggatg atggagatg cagccttgat catgtgactt gcagcatgat	4020
cacctactgc cttctgagta gaagaactca ctgcagagca gtttacctca tttgaccta	4080
gttgcattgt atcgaaatgt ctgagtcact gcgtgcagag gcagaagcaa attgcagaac	4140
tgcacaggggt ggtgggtcct tttggggctt tcctagtcac tcagactgac cggcccccgc	4200
ttcacacggg cgcttcaat agtttaaga ttattttaa atgtgtatTT tagcctttta	4260
ataaaaaatct caatcaatta cttcttgcc tattttggtt ttacaaaaac acccactatc	4320
aaggagtgcc tgtctgcgga cgattaaat gctgtccgg gcgtaccgta aactgagagc	4380
ttgctgtacc tttgccgtt gtccagtgtt cccaaaccaca ttgtgttagtt tggggctgtt	4440
ccctgcccgt aagcacagag gagatgggtg tacctgttt gaaaatgtgt atgttagactg	4500
agcctgacta tggaaagggt tatgcttgcc tgtgaccatc acgtgtacct gtcgcgcgt	4560

taccatctgt accgaagaag tagctttcc tccatggcta aaccaccac cgtgtacagt 4620
 gctctatct actgcattca tttacttg cacagtgacc ttgttagccac ctgaggaagc 4680
 acccatgttt ccgtttggtc tcagatgtac ctagttgtgc ccgtgttttggttttat 4740
 tcaatctggc atgtcttcac accataaact agtaagacgc caactgcccggcggttacg 4800
 atcatcagta cccaccgtct tagtctctgt tacgtgaagt ttattccagt tgcttttat 4860
 ggaatatctt gaacaagtaa tcttcttgac aagaaagaat gtatagaagt ctccctgcaa 4920
 ttaatttccc agtgtttaca ttttttaact agactgtggg ggtgtctaca gattaatatg 4980
 aaatggcgct cctggtccgt gtgtgtgtta acttgtgtcg tagctgaagc cgtgtgtcct 5040
 tagatattag ttggaaagtcg ggaagagaat tcgatataaa gctt 5084

<210> 2
 <211> 3642
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(3642)
 <223> Mouse Esel

<400> 2
 atg gct cag ttt ccc aca cct ttc ggt ggt agc ctg gat gtc tgg gcc 48
 Met Ala Gln Phe Pro Thr Pro Phe Gly Gly Ser Leu Asp Val Trp Ala
 1 5 10 15

ata act gtg gag gaa agg gcc aag cat gac cag cag ttc ctt agc ctg 96
 Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu
 20 25 30

aag ccg ata gcg gga ttt att act ggt gat caa gcg agg aac ttt ttt 144
 Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
 35 40 45

ttc caa tct ggg tta cct cag cct gtc tta gca caa ata tgg gcg cta 192
 Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
 50 55 60

gcg gac atg aat aac gat gga agg atg gat caa gtg gaa ttt tcc ata 240
 Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile
 65 70 75 80

gcc atg aag ctt atc aaa ctg aag cta caa gga tat cag ctc ccc tcc 288
 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser
 85 90 95

aca ctt ccc cct gtc atg aaa cag caa cca gtg gct att tcc agt gca 336
 Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala
 100 105 110

cca gca ttt ggt ata gga ggg att gct agc atg cca cca ctc aca gct 384

Pro Ala Phe Gly Ile Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala			
115	120	125	
gtt gct cct gtg cca atg ggc tcc att cca gtt ggt gaa atg tct cca			432
Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro			
130	135	140	
ccc tta gta tct tct gtc cct cca gca gca gtg cct ccc ctg gct aac			480
Pro Leu Val Ser Ser Val Pro Pro Ala Ala Val Pro Pro Leu Ala Asn			
145	150	155	160
ggg gct cct ccc gtc ata cag cct ctg cct gcg ttt gcg cat cct gca			528
Gly Ala Pro Pro Val Ile Gln Pro Leu Pro Ala Phe Ala His Pro Ala			
165	170	175	
gcc aca tgg cca aag agt tct tcc agc aga tct ggt cca ggg tca			576
Ala Thr Trp Pro Lys Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser			
180	185	190	
caa tta aac act aag tta cag aag gca caa tca ttc gat gtc gcc agc			624
Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser			
195	200	205	
gcc cct cca gca gca gaa tgg gct gtg cct cag tca tca agg ctg aaa			672
Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys			
210	215	220	
tac agg cag tta ttc aac agc cac gac aaa act atg agt gga cac tta			720
Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu			
225	230	235	240
aca ggt ccc cag gca aga act att ctc atg caa tca agt tta ccc cag			768
Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln			
245	250	255	
gct cag ctg gct tca ata tgg aat ctt tct gac att gat caa gat gga			816
Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly			
260	265	270	
aaa ctc act gca gaa gaa ttt atc cta gct atg cac cta att gat gtt			864
Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val			
275	280	285	
gcc atg tct ggt cag cca ctg ccg ccc gtc ctg cct cca gaa tac atc			912
Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile			
290	295	300	
cct cct tcc ttc aga aga gtt cgc tcc ggc agt ggg atg tcc gtc ata			960
Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile			
305	310	315	320
agc tct tct gtg gat cag agg ctg cct gag gag ccg tcg tca gag			1008
Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu			
325	330	335	
gat gag cag cca gag aag aaa ctg cct gtg aca ttt gaa gat aag			1056
Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys			
340	345	350	
aag cgg gag aac ttc gag cga ggc agt gtg gag ctg gag aag cgc cgc			1104
Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg			

355	360	365	
caa gcg ctc ttg gag cag cag cgc aaa gag cag gag cgg ttg gct cag Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln 370	375	380	1152
ctg gag cgc gcc gag cag gag agg aaa gag cgg gag cgc cag gag cag Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln 385	390	395	1200
gag gcc aag cgg cag ctg gag aag cag ctg gag aag cag cgg Glu Ala Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln Arg 405	410	415	1248
gag ctg gag cgg cag cga gag gag agg aag gag atc gag agg Glu Leu Glu Arg Gln Arg Glu Glu Arg Arg Lys Glu Ile Glu Arg 420	425	430	1296
cgc gag gcc gca aaa cgg gaa ctg gaa agg cag cga caa ctt gaa tgg Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp 435	440	445	1344
gaa cgg aac cgg aga cag gaa ctc ctg aat cag agg aac aag gag cag Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln 450	455	460	1392
gag ggc acc gtg gtc ctg aag gca agg agg aag act ctg gag ttt gag Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu 465	470	475	1440
tta gaa gct ctg aat gac aaa aag cat cag cta gaa gga aaa ctt cag Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln 485	490	495	1488
gat atc agg tgt cga ctg gca acc cag agg caa gaa att gag agc acg Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr 500	505	510	1536
aac aag tct aga gag cta aga att gct gaa atc acc cac tta cag cag Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln 515	520	525	1584
cag ttg cag gaa tct cag caa atg ctt gga aga ctt att cca gag aaa Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys 530	535	540	1632
cag ata ctc agt gac cag tta aaa caa gtc cag cag aac agt ttg cat Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His 545	550	555	1680
aga gac tcg ctt ctt acc ctc aaa aga gcc ttg gaa gca aag gag ctg Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu 565	570	575	1728
gcc cgg cag ctc cgg gag cag ctg gac gag gtg gag aga gag acc Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr 580	585	590	1776
agg tca aag ctg cag gag att gat gtt ttc aac aac cag ctg aag gaa Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu 595	600	605	1824

ctg aga gag ata cat agc aaa cag caa ctc cag aag cag agg tcc ctg	610	615	620	1872
Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu				
gag gca gcg cga ctg aag cag aaa gag cag gag agg aag agc ctg gag	625	630	635	1920
Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu				
tta gag aag caa aag gaa gac gct cag aga cga gtt cag gaa agg gac	645	650	655	1968
Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp				
aag caa tgg ctg gag cat gtg cag cag gag cag cca cgc ccc cgg	660	665	670	2016
Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg				
aaa ccc cac gag gag gac aga ctg aag agg gaa gac agt gtc agg aag	675	680	685	2064
Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys				
aag gag gcg gaa gag aga gcc aag ccc gaa atg caa gac aag cag agt	690	695	700	2112
Lys Glu Ala Glu Glu Arg Ala Lys Pro Glu Met Gln Asp Lys Gln Ser				
cgg ctt ttc cat ccg cat cag gag cca gct aag ctg gcc acc cag gca	705	710	715	2160
Arg Leu Phe His Pro His Gln Glu Pro Ala Lys Leu Ala Thr Gln Ala				
ccc tgg tct acc aca gag aaa ggc ccg ctt acc att tct gca cag gag	725	730	735	2208
Pro Trp Ser Thr Thr Glu Lys Gly Pro Leu Thr Ile Ser Ala Gln Glu				
agt gta aaa gtg gta tat tac cga gcg ctg tac ccc ttt gaa tcc aga	740	745	750	2256
Ser Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg				
agt cac gat gag atc acc atc cag cca gga gat ata gtc atg gtg gat	755	760	765	2304
Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp				
gaa agc cag act gga gag cca gga tgg ctt gga gga gag ctg aaa ggg	770	775	780	2352
Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly				
aag acg gga tgg ttc cct gca aac tat gca gaa aag att cca gaa aat	785	790	795	2400
Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro Glu Asn				
gag gtt ccc act cca gcc aaa cca gtg acc gat ctg aca tct gcc cct	805	810	815	2448
Glu Val Pro Thr Pro Ala Lys Pro Val Thr Asp Leu Thr Ser Ala Pro				
gcc ccc aaa ctg gct ctg cgt gag acc cct gct cct ttg cca gtg acc	820	825	830	2496
Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Pro Val Thr				
tct tct gag ccc tcc aca acc ccc aac aac tgg gca gac ttc agt tcc	835	840	845	2544
Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe Ser Ser				

acg tgg ccc agc agc tca aac gag aag cca gaa acg gac aac tgg gat	2592
Thr Trp Pro Ser Ser Ser Asn Glu Lys Pro Glu Thr Asp Asn Trp Asp	
850 855 860	
acg tgg gcg gct cag cct tct ctg acc gta cct agt gct ggc cag tta	2640
Thr Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly Gln Leu	
865 870 875 880	
cgg cag aga tca gcc ttt acc cca gcc aca gcc act ggc tcc tcc cca	2688
Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser Ser Pro	
885 890 895	
tct ccc gtc ctg ggc cag ggt gaa aag gtg gaa ggg cta caa gcg caa	2736
Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln Ala Gln	
900 905 910	
gcc ctg tat ccc tgg aga gcc aaa aaa gac aac cac tta aat ttt aac	2784
Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn Phe Asn	
915 920 925	
aaa agt gac gtc atc acc gtt ctg gaa cag caa gac atg tgg tgg ttt	2832
Lys Ser Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp Trp Phe	
930 935 940	
gga gaa gtt caa ggt cag aag ggt tgg ttc ccc aag tct tac gtg aaa	2880
Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr Val Lys	
945 950 955 960	
ctc att tca ggg ccc gta agg aaa tcc aca agc atc gat act ggc cct	2928
Leu Ile Ser Gly Pro Val Arg Lys Ser Thr Ser Ile Asp Thr Gly Pro	
965 970 975	
act gaa agt cct gct agt cta aag aga gtg gct tcc ccg gcc gcc aag	2976
Thr Glu Ser Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala Ala Lys	
980 985 990	
cca gcc att ccc gga gaa gag ttt att gcc atg tac aca tac gag agt	3024
Pro Ala Ile Pro Gly Glu Glu Phe Ile Ala Met Tyr Thr Tyr Glu Ser	
995 1000 1005	
tct gag caa gga gat tta acc ttt cag caa ggg gat gtg att gtg	3069
Ser Glu Gln Gly Asp Leu Thr Phe Gln Gln Gly Asp Val Ile Val	
1010 1015 1020	
gtt acc aag aaa gat ggt gac tgg tgg acg gga acg gtg ggc gac	3114
Val Thr Lys Lys Asp Gly Asp Trp Trp Thr Gly Thr Val Gly Asp	
1025 1030 1035	
aag tcc gga gtc ttc cct tct aac tat gtg agg ctt aaa gat tca	3159
Lys Ser Gly Val Phe Pro Ser Asn Tyr Val Arg Leu Lys Asp Ser	
1040 1045 1050	
gag ggc tct gga act gct ggg aaa aca ggg agt tta gga aaa aaa	3204
Glu Gly Ser Gly Thr Ala Gly Lys Thr Gly Ser Leu Gly Lys Lys	
1055 1060 1065	
cct gaa att gcc cag gtt att gct tcc tac gct gct act ggt ccc	3249
Pro Glu Ile Ala Gln Val Ile Ala Ser Tyr Ala Ala Thr Gly Pro	
1070 1075 1080	
gaa caa ctc acc ctg gct cct ggg cag ctg att ctg atc cgg aaa	3294

Glu Gln Leu Thr Leu Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys			
1085	1090	1095	
aag aac cca ggt gga tgg tgg gaa gga gaa ctg caa gct cga ggg			3339
Lys Asn Pro Gly Gly Trp Trp Glu Gly Glu Leu Gln Ala Arg Gly			
1100	1105	1110	
aaa aag cgc cag ata ggg tgg ttt cca gca aat tat gtc aaa ctt			3384
Lys Lys Arg Gln Ile Gly Trp Phe Pro Ala Asn Tyr Val Lys Leu			
1115	1120	1125	
cta agc ccc gga aca agc aaa atc acc cca act gag cta ccc aag			3429
Leu Ser Pro Gly Thr Ser Lys Ile Thr Pro Thr Glu Leu Pro Lys			
1130	1135	1140	
acc gca gtg cag cca gca gtg tgc cag gtg atc ggg atg tac gat			3474
Thr Ala Val Gln Pro Ala Val Cys Gln Val Ile Gly Met Tyr Asp			
1145	1150	1155	
tac acc gcc cag aac gat gac gaa cta gcc ttc agc aaa ggc cag			3519
Tyr Thr Ala Gln Asn Asp Asp Glu Leu Ala Phe Ser Lys Gly Gln			
1160	1165	1170	
atc atc aac gtc ctc aac aag gag gac ccg gac tgg tgg aaa gga			3564
Ile Ile Asn Val Leu Asn Lys Glu Asp Pro Asp Trp Trp Lys Gly			
1175	1180	1185	
gaa gtc agt ggg caa gtt ggg ctc ttc cca tcc aat tat gta aag			3609
Glu Val Ser Gly Gln Val Gly Leu Phe Pro Ser Asn Tyr Val Lys			
1190	1195	1200	
ctg acc aca gac atg gac ccc agc cag caa tga			3642
Leu Thr Thr Asp Met Asp Pro Ser Gln Gln			
1205	1210		

<210> 3
 <211> 1213
 <212> PRT
 <213> Mus musculus

<400> 3

Met Ala Gln Phe Pro Thr Pro Phe Gly Gly Ser Leu Asp Val Trp Ala
 1 5 10 15

Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu
 20 25 30

Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
 35 40 45

Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
 50 55 60

Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile
 65 70 75 80

Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser
85 90 95

Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala
100 105 110

Pro Ala Phe Gly Ile Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala
115 120 125

Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro
130 135 140

Pro Leu Val Ser Ser Val Pro Pro Ala Ala Val Pro Pro Leu Ala Asn
145 150 155 160

Gly Ala Pro Pro Val Ile Gln Pro Leu Pro Ala Phe Ala His Pro Ala
165 170 175

Ala Thr Trp Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser
180 185 190

Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser
195 200 205

Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys
210 215 220

Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu
225 230 235 240

Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln
245 250 255

Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly
260 265 270

Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val
275 280 285

Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile
290 295 300

Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile
305 310 315 320

Ser Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu
325 330 335

Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys
340 345 350

Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg
355 360 365

Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln
370 375 380

Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln
385 390 395 400

Glu Ala Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln Arg
405 410 415

Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg
420 425 430

Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp
435 440 445

Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln
450 455 460

Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu
465 470 475 480

Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln
485 490 495

Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr
500 505 510

Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln
515 520 525

Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys
530 535 540

Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His
545 550 555 560

Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu
565 570 575

Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr
580 585 590

Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu
595 600 605

Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu
610 615 620

Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu
625 630 635 640

Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp
645 650 655

Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg
660 665 670

Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys
675 680 685

Lys Glu Ala Glu Glu Arg Ala Lys Pro Glu Met Gln Asp Lys Gln Ser
690 695 700

Arg Leu Phe His Pro His Gln Glu Pro Ala Lys Leu Ala Thr Gln Ala
705 710 715 720

Pro Trp Ser Thr Thr Glu Lys Gly Pro Leu Thr Ile Ser Ala Gln Glu
725 730 735

Ser Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg
740 745 750

Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp
755 760 765

Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly
770 775 780

Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro Glu Asn
785 790 795 800

Glu Val Pro Thr Pro Ala Lys Pro Val Thr Asp Leu Thr Ser Ala Pro

805

810

815

Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Pro Val Thr
820 825 830

Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe Ser Ser
835 840 845

Thr Trp Pro Ser Ser Asn Glu Lys Pro Glu Thr Asp Asn Trp Asp
850 855 860

Thr Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly Gln Leu
865 870 875 880

Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser Ser Pro
885 890 895

Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln Ala Gln
900 905 910

Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn Phe Asn
915 920 925

Lys Ser Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp Trp Phe
930 935 940

Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr Val Lys
945 950 955 960

Leu Ile Ser Gly Pro Val Arg Lys Ser Thr Ser Ile Asp Thr Gly Pro
965 970 975

Thr Glu Ser Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala Ala Lys
980 985 990

Pro Ala Ile Pro Gly Glu Glu Phe Ile Ala Met Tyr Thr Tyr Glu Ser
995 1000 1005

Ser Glu Gln Gly Asp Leu Thr Phe Gln Gln Gly Asp Val Ile Val
1010 1015 1020

Val Thr Lys Lys Asp Gly Asp Trp Trp Thr Gly Thr Val Gly Asp
1025 1030 1035

Lys Ser Gly Val Phe Pro Ser Asn Tyr Val Arg Leu Lys Asp Ser
1040 1045 1050

Glu Gly Ser Gly Thr Ala Gly Lys Thr Gly Ser Leu Gly Lys Lys
1055 1060 1065

Pro Glu Ile Ala Gln Val Ile Ala Ser Tyr Ala Ala Thr Gly Pro
1070 1075 1080

Glu Gln Leu Thr Leu Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys
1085 1090 1095

Lys Asn Pro Gly Gly Trp Trp Glu Gly Glu Leu Gln Ala Arg Gly
1100 1105 1110

Lys Lys Arg Gln Ile Gly Trp Phe Pro Ala Asn Tyr Val Lys Leu
1115 1120 1125

Leu Ser Pro Gly Thr Ser Lys Ile Thr Pro Thr Glu Leu Pro Lys
1130 1135 1140

Thr Ala Val Gln Pro Ala Val Cys Gln Val Ile Gly Met Tyr Asp
1145 1150 1155

Tyr Thr Ala Gln Asn Asp Asp Glu Leu Ala Phe Ser Lys Gly Gln
1160 1165 1170

Ile Ile Asn Val Leu Asn Lys Glu Asp Pro Asp Trp Trp Lys Gly
1175 1180 1185

Glu Val Ser Gly Gln Val Gly Leu Phe Pro Ser Asn Tyr Val Lys
1190 1195 1200

Leu Thr Thr Asp Met Asp Pro Ser Gln Gln
1205 1210

<210> 4

<211> 4625

<212> DNA

<213> Mus musculus

<400> 4
cccttccttt ccttttttg tgttcgctt cggccgtgcc ggctgagagc ccagcagccg 60
tgacaggctg cgcaacaggt tcgctcgcc cggcctgacg actgaccgg cggcggccgc 120
cgcggcacgg cagggtcttc ccggagctt gccgcgcaca cgcgcgggtg tcgaggagcg 180
cgcgggtcg cgccgggacg tgcgcgaggc gccagatggc tgagagctgc aagaagaagt 240
caggatcatg atggctcagt ttcccacagc gatgaatgga gggccaaata tgtggctat 300

tacatctgaa gaacgtacta agcatgataa acagtttat aacctcaaac cttcaggagg 360
ttacataaca ggtgatcaag cccgtacttt tttcctacag tcaggtctgc cggccccggt 420
tttagctgaa atatgggcct tatcagatct gaacaaggat gggaaagatgg accagcaaga 480
gttctctata gctatgaaac tcatcaagtt aaagttgcag gccaacacgc tgcctgtagt 540
cctccctcct atcatgaaac aaccccttat gttctctcca ctaatctctg ctcgtttgg 600
gatggaaagc atgcccatac tgtccattca tcagccattg cctccagttg cacctatagc 660
aacacccttgc tcttctgcta cgtcagggac cagtattcct cccctaattga tgcctgtcc 720
cctagtgccct tctgttagta catcctcatt accaaatgga actgccagtc tcattcagcc 780
tttatccatt ccttattctt cttcaacatt gcctcatgca tcatcttaca gcctgatgat 840
gggaggattt ggtggtgcta gtatccagaa ggcccagttt ctgattgatt taggatctag 900
tagctcaact tcctcaactg cttccctctc agggaaactca cctaagacag ggacctcaga 960
gtggcagtt cctcagcctt caagattaaa gtatcgcaaa aaatttaata gtctagacaa 1020
aggcatgagc ggataacctct caggtttca agctagaaat gcccttcttc agtcaaatct 1080
ctctcaact cagctagcta ctatttggac tctggctgac atcgatggtg acggacagtt 1140
gaaagctgaa gaatttatttc tggcgatgca cctcaactgac atggccaaag ctggacagcc 1200
actaccactg acgttgcctc ccgagcttgt ccctccatct ttcagagggg gaaagcaagt 1260
tgattctgtt aatggaaactc tgccttcata tcagaaaaca caagaagaag agcctcagaa 1320
gaaactgcca gttacttttggaggacaaacg gaaagccaaac tatgaacgag gaaacatggaa 1380
gctggagaag cgacgccaag tggatggaa gcagcagcag agggaggctg aacgccaagc 1440
ccagaaagag aaggaagagt gggagcggaa acagagagaa ctgcaagagc aagaatggaa 1500
gaagcagctg gagttggaga aacgcttgaa gaaacagaga gagctggaga gacagcggaa 1560
ggaagagagg agaaaggaga tagaaagacg agaggcagca aaacaggago ttgagagaca 1620
acgccgttta gaatggaaa gactccgtcg gcaggagctg ctcagtcaga agaccaggaa 1680
acaagaagac attgtcaggc tgagctccag aaagaaaagt ctccacctgg aactggaaagc 1740
agtgaatggaa aacatcagc agatctcagg cagactacaa gatgtccaaa tcagaaagca 1800
aacacaaaag actgagctag aagttttggaa taaacagtgt gacctggaaa ttatggaaat 1860
caaacaactt caacaagagc ttaaggaata tcaaaataag cttatctatc tggccctgaa 1920
gaagcagcta ttaaacgaaa gaattaaaaa catgcagctc agtaacacac ctgattcagg 1980
gatcagttta cttcataaaaa agtcatcaga aaaggaagaa ttatggccaaa gacttaaaga 2040
acaatttagat gctcttgaaa aagaaactgc atctaagctc tcagaaatgg attcattaa 2100

caatcagctg aaggaactca gagaaagcta taatacacag cagttagccc ttgaacaact 2160
 tcataaaatc aaacgtgaca aattgaagga aatcgaaaga aaaagattag agcaaattca 2220
 aaaaaagaaa ctagaagatg aggctgcaag gaaagcaaag caagggaaag aaaaacttgc 2280
 gagagaaaatg attagaaagg aagaagagga aaagcaaaaa cgactccagg aagaaaagtc 2340
 acaggacaaa actcaagaag aggaacgaaa agctgaggca aaacaaagtg agacagccag 2400
 tgctttggtg aattacagag cactgtaccc ttttgaagca agaaaccatg atgagatgag 2460
 ttttagttct ggggatataa ttcaggttga tgaaaaact gtaggagagc ctggttggct 2520
 ttatggtagt tttcagggaa agtttgctg gttccctgc aactatgttag aaaaagtgt 2580
 gtcaagtgaa aaagctctgt ctccctaagaa ggccttactt cctcctacag tgtctctctc 2640
 tgctaccta acttcttccc agccaccagc atcagtgact gattatcaca atgtatcctt 2700
 ctcaaacctt actgttaata caacatggca gcagaagtca gctttaccc gcactgtgtc 2760
 ccctggatct gtgtccccca ttcacggaca ggggcaggct gtagaaaacc tgaaagccca 2820
 ggcctttgt tcctggacgg caaagaagga gaaccacctg aacttctcaa agcacgacgt 2880
 catcaactgtc ctggaggcagc agaaaaactg gtggtttggg gaggtgcacg gaggaagagg 2940
 atggttcccc aagtcttatg tcaagctcat tcctggaaat gaagtacagc gaggagagcc 3000
 agaagctttg tatgcagctg tgactaagaa acctaccc acagcctatc cagttaccc 3060
 cacagctat ccagttggag aagactacat tgcactttat tcatactcaa gtgttagagcc 3120
 cggggatttg actttcactg aaggtgaaga aattcttagtg acccagaaag atggagagtg 3180
 gtggacagga agtattggag agagaactgg aatcttcccg tccaactacg tcagaccaaa 3240
 gcatcaagag aattttggga atgctagcaa atctggagca tcaaacaaaa aacccgagat 3300
 cgctcaagta acttcagcat atgctgcttc agggactgag cagctcagcc ttgcggcagg 3360
 acagttataa ttaatcttaa agaaaaacac aagcgggtgg tggcaaggag agctacaggc 3420
 cagagggaaag aaacgacaga agggatggtt tcctggcagc catgtaaagc tgcttagtcc 3480
 aagcagtgaa agaaccatgc ctactttca cgctgtatgt caagtgattg ctatgtatga 3540
 ctacatggcg aataacgaag atgagctaa tttctccaaa ggacagctga ttaatgttat 3600
 gaacaaagat gaccctgact ggtggcaagg agaaaccaat ggtctgactg gtctttcc 3660
 ttcaaaactat gttaagatga caacagactc agatccaagt caacagtggt gtgctgaccc 3720
 ccaagccctg gacacaatgc agcctacgga gaggaagcga cagggctaca ttcacgagct 3780
 cattcagaca gaggagcggt acatggacga cctgcaactt tttgaacaaa aaactctcct 3840
 ttgagggcct ggggaagcca gaaccagggg agctgcccac aaggctgggt ctaaagacag 3900
 attttgctct cccaggacag aggagcatca catcggcttc atccatccaa acaagccaca 3960

ctcgctgggc ctggtatattt attgcaccac taaaattgct agcaatctat gcaaacatga	4020
tctttttaaa caaacgccac agcacagtgc cttgtactag tgttaacctg ttcagctgtg	4080
tttagatgcca gggtttccat tttcagggct ataaaagtat tatgtggaa atgagacatc	4140
agaccaccgg acgttaccac ttggcaaatc tgtccactgt ggagttggtg atgttggAAC	4200
cattccacac tatgtgacct ctgctgggtc acacactcag gaggtgaagg gctgagatga	4260
aatgctgcag ccttggggct tgtgcagcct gatactgaaa tagcatccac ttgtgcactg	4320
aataaaataga aacttgatcg ttttattctg actagatatt atcattctct gctaagacaa	4380
tatagttga aatattatag tttgaatata aggaggaaag cttgatgtac tttaaatata	4440
ctgtgaactc taataatgtg gggatatttt tcaactttaa tttcttaag tataaattat	4500
ttatgtaaat tctttgtttt gcataattca tagAACatgc atcttaagc tttatcattg	4560
ccaacaatgt acagaaagag aataaaagta taagtttatg aatgtaaaaa aaaaaaaaaa	4620
aaaaaa	4625

```
<210> 5
<211> 3594
<212> DNA
<213> Mus musculus
```

```

<220>
<221> CDS
<222> (1)..(3594)
<223> Mouse Ese2

<400> 5
atg gct cag ttt ccc aca gca atg aat gga ggg cca aat atg tgg gct 48
Met Ala Gln Phe Pro Thr Ala Met Asn Gly Gly Pro Asn Met Trp Ala
1 5 10 15

att aca tct gaa gaa cgt act aag cat gat aaa cag ttt gat aac ctc 96
Ile Thr Ser Glu Glu Arg Thr Lys His Asp Lys Gln Phe Asp Asn Leu
20 25 30

aaa cct tca gga ggt tac ata aca ggt gat caa gcc cgt act ttt ttc 144
Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe
35 40 45

cta cag tca ggt ctg ccg gcc ccg gtt tta gct gaa ata tgg gcc tta 192
Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu
50 55 60

tca gat ctg aac aag gat ggg aag atg gac cag caa gag ttc tct ata 240
Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile
65 70 75 80

gct atg aaa ctc atc aag tta aag ttg cag ggc caa cag ctg cct gta 288
Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val
85 90 95

```

gtc ctc cct ctc atc atg aaa caa ccc cct atg ttc tct cca cta atc		336	
Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile			
100	105	110	
tct gct cgt ttt ggg atg gga agc atg ccc aat ctg tcc att cat cag		384	
Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln			
115	120	125	
cca ttg cct cca gtt gca cct ata gca aca ccc ttg tct tct gct acg		432	
Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr			
130	135	140	
tca ggg acc agt att cct ccc cta atg atg cct gct ccc cta gtg cct		480	
Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro			
145	150	155	160
tct gtt agt aca tcc tca tta cca aat gga act gcc agt ctc att cag		528	
Ser Val Ser Thr Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln			
165	170	175	
cct tta tcc att cct tat tct tct tca aca ttg cct cat gca tca tct		576	
Pro Leu Ser Ile Pro Tyr Ser Ser Thr Leu Pro His Ala Ser Ser			
180	185	190	
tac agc ctg atg atg gga gga ttt ggt ggt gct agt atc cag aag gcc		624	
Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala			
195	200	205	
cag tct ctg att gat tta gga tct agt agc tca act tcc tca act gct		672	
Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Thr Ser Ser Thr Ala			
210	215	220	
tcc ctc tca ggg aac tca cct aag aca ggg acc tca gag tgg gca gtt		720	
Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val			
225	230	235	240
cct cag cct tca aga tta aag tat cgg caa aaa ttt aat agt cta gac		768	
Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp			
245	250	255	
aaa ggc atg agc gga tac ctc tca ggt ttt caa gct aga aat gcc ctt		816	
Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu			
260	265	270	
ctt cag tca aat ctc tct caa act cag cta gct act att tgg act ctg		864	
Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu			
275	280	285	
gct gac atc gat ggt gac gga cag ttg aaa gct gaa gaa ttt att ctg		912	
Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu			
290	295	300	
gcg atg cac ctc act gac atg gcc aaa gct gga cag cca cta cca ctg		960	
Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu			
305	310	315	320
acg ttg cct ccc gag ctt gtc cct cca tct ttc aga ggg gga aag caa		1008	
Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln			
325	330	335	

gtt gat tct gtt aat gga act ctg cct tca tat cag aaa aca caa gaa	1056
Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu	
340 345 350	
gaa gag cct cag aag aaa ctg cca gtt act ttt gag gac aaa cgg aaa	1104
Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys	
355 360 365	
gcc aac tat gaa cga gga aac atg gag ctg gag aag cga cgc caa gtg	1152
Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val	
370 375 380	
ttg atg gag cag cag cag agg gag gct gaa cgc aaa gcc cag aaa gag	1200
Leu Met Glu Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu	
385 390 395 400	
aag gaa gag tgg gag cgg aaa cag aga gaa ctg caa gag caa gaa tgg	1248
Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp	
405 410 415	
aag aag cag ctg gag ttg gag aaa cgc ttg gag aaa cag aga gag ctg	1296
Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu	
420 425 430	
gag aga cag cgg gag gaa gag agg aga aag gag ata gaa aga cga gag	1344
Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu	
435 440 445	
gca gca aaa cag gag ctt gag aga caa cgc cgt tta gaa tgg gaa aga	1392
Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg	
450 455 460	
ctc cgt cgg cag gag ctg ctc agt cag aag acc agg gaa caa gaa gac	1440
Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp	
465 470 475 480	
att gtc agg ctg agc tcc aga aag aaa agt ctc cac ctg gaa ctg gaa	1488
Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu	
485 490 495	
gca gtg aat gga aaa cat cag cag atc tca ggc aga cta caa gat gtc	1536
Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val	
500 505 510	
caa atc aga aag caa aca caa aag act gag cta gaa gtt ttg gat aaa	1584
Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys	
515 520 525	
cag tgt gac ctg gaa att atg gaa atc aaa caa ctt caa caa gag ctt	1632
Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Glu Leu	
530 535 540	
aag gaa tat caa aat aag ctt atc tat ctg gtc cct gag aag cag cta	1680
Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu	
545 550 555 560	
tta aac gaa aga att aaa aac atg cag ctc agt aac aca cct gat tca	1728
Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser	
565 570 575	
ggg atc agt tta ctt cat aaa aag tca tca gaa aag gaa tta tgc	1776

Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys			
580	585	590	
caa aga ctt aaa gaa caa tta gat gct ctt gaa aaa gaa act gca tct			1824
Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser			
595	600	605	
aag ctc tca gaa atg gat tca ttt aac aat cag ctg aag gaa ctc aga			1872
Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg			
610	615	620	
gaa agc tat aat aca cag cag tta gcc ctt gaa caa ctt cat aaa atc			1920
Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile			
625	630	635	640
aaa cgt gac aaa ttg aag gaa atc gaa aga aaa aga tta gag caa att			1968
Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile			
645	650	655	
caa aaa aag aaa cta gaa gat gag gct gca agg aaa gca aag caa gga			2016
Gln Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly			
660	665	670	
aaa gaa aac ttg tgg aga gaa agt att aga aag gaa gaa gag gaa aag			2064
Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Lys			
675	680	685	
caa aaa cga ctc cag gaa aag tca cag gac aaa act caa gaa gag			2112
Gln Lys Arg Leu Gln Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu			
690	695	700	
gaa cga aaa gct gag gca aaa caa agt gag aca gcc agt gct ttg gtg			2160
Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val			
705	710	715	720
aat tac aga gca ctg tac cct ttt gaa gca aga aac cat gat gag atg			2208
Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met			
725	730	735	
agt ttt agt tct ggg gat ata att cag gtt gat gaa aaa act gta gga			2256
Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly			
740	745	750	
gag cct ggt tgg ctt tat ggt agt ttt cag gga aag ttt ggc tgg ttc			2304
Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe			
755	760	765	
ccc tgc aac tat gta gaa aaa gtg ctg tca agt gaa aaa gct ctg tct			2352
Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser			
770	775	780	
cct aag aag gcc tta ctt cct cct aca gtg tct ctc tct gct acc tca			2400
Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser			
785	790	795	800
act tct tcc cag cca cca gca tca gtg act gat tat cac aat gta tcc			2448
Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser			
805	810	815	
ttc tca aac ctt act gtt aat aca aca tgg cag cag aag tca gct ttt			2496
Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe			

820	825	830	
acc cgc act gtg tcc cct gga tct gtg tcc ccc att cac gga cag ggg Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly	835	840	2544
		845	
cag gct gta gaa aac ctg aaa gcc cag gcc ctt tgt tcc tgg acg gca Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala	850	855	2592
		860	
aag aag gag aac cac ctg aac ttc tca aag cac gac gtc atc act gtc Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val	865	870	2640
		875	880
ctg gag cag cag gaa aac tgg tgg ttt ggg gag gtg cac gga gga aga Leu Glu Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg	885	890	2688
		895	
gga tgg ttc ccc aag tct tat gtc aag ctc att cct ggg aat gaa gta Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val	900	905	2736
		910	
cag cga gga gag cca gaa gct ttg tat gca gct gtg act aag aaa cct Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro	915	920	2784
		925	
acc tcc aca gcc tat cca gtt acc tcc aca gcc tat cca gtt gga gaa Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu	930	935	2832
		940	
gac tac att gca ctt tat tca tac tca agt gta gag ccc ggg gat ttg Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Val Glu Pro Gly Asp Leu	945	950	2880
		955	960
act ttc act gaa ggt gaa gaa att cta gtg acc cag aaa gat gga gag Thr Phe Thr Glu Gly Glu Ile Leu Val Thr Gln Lys Asp Gly Glu	965	970	2928
		975	
tgg tgg aca gga agt att gga gag aga act gga atc ttc ccg tcc aac Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn	980	985	2976
		990	
tac gtc aga cca aag gat caa gag aat ttt ggg aat gct agc aaa tct Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser	995	1000	3024
		1005	
gga gca tca aac aaa aaa ccc gag atc gct caa gta act tca gca Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala	1010	1015	3069
		1020	
tat gct gct tca ggg act gag cag ctc agc ctt gcg cca gga cag Tyr Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln	1025	1030	3114
		1035	
tta ata tta atc tta aag aaa aac aca agc ggg tgg tgg caa gga Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly	1040	1045	3159
		1050	
gag cta cag gcc aga ggg aag aaa cga cag aag gga tgg ttt cct Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro	1055	1060	3204
		1065	

gcc agc cat gta aag ctg cta ggt cca agc agt gaa aga acc atg		3249
Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met		
1070	1075	1080
cct act ttt cac gct gta tgt caa gtg att gct atg tat gac tac		3294
Pro Thr Phe His Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr		
1085	1090	1095
atg gcg aat aac gaa gat gag ctc aat ttc tcc aaa gga cag ctg		3339
Met Ala Asn Asn Glu Asp Glu Leu Asn Phe Ser Lys Gly Gln Leu		
1100	1105	1110
att aat gtt atg aac aaa gat gac cct gac tgg tgg caa gga gaa		3384
Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu		
1115	1120	1125
acc aat ggt ctg act ggt ctc ttt cct tca aac tat gtt aag atg		3429
Thr Asn Gly Leu Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met		
1130	1135	1140
aca aca gac tca gat cca agt caa cag tgg tgt gct gac ctc caa		3474
Thr Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln		
1145	1150	1155
gcc ctg gac aca atg cag cct acg gag agg aag cga cag ggc tac		3519
Ala Leu Asp Thr Met Gln Pro Thr Glu Arg Lys Arg Gln Gly Tyr		
1160	1165	1170
att cac gag ctc att cag aca gag gag cgg tac atg gac gac ctg		3564
Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr Met Asp Asp Leu		
1175	1180	1185
caa ctt ttt gaa caa aaa act ctc ctt tga		3594
Gln Leu Phe Glu Gln Lys Thr Leu Leu		
1190	1195	
<210> 6		
<211> 1197		
<212> PRT		
<213> Mus musculus		
<400> 6		
Met Ala Gln Phe Pro Thr Ala Met Asn Gly Gly Pro Asn Met Trp Ala		
1 5 10 15		
Ile Thr Ser Glu Glu Arg Thr Lys His Asp Lys Gln Phe Asp Asn Leu		
20 25 30		
Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe		
35 40 45		
Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu		
50 55 60		

Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile
65 70 75 80

Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val
85 90 95

Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile
100 105 110

Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln
115 120 125

Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr
130 135 140

Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro
145 150 155 160

Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln
165 170 175

Pro Leu Ser Ile Pro Tyr Ser Ser Thr Leu Pro His Ala Ser Ser
180 185 190

Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala
195 200 205

Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Thr Ser Ser Thr Ala
210 215 220

Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val
225 230 235 240

Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp
245 250 255

Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu
260 265 270

Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu
275 280 285

Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu
290 295 300

Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu

305 310 315 320

Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln
325 330 335

Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu
340 345 350

Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys
355 360 365

Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val
370 375 380

Leu Met Glu Gln Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu
385 390 395 400

Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp
405 410 415

Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu
420 425 430

Glu Arg Gln Arg Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu
435 440 445

Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg
450 455 460

Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp
465 470 475 480

Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu
485 490 495

Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val
500 505 510

Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys
515 520 525

Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu
530 535 540

Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu
545 550 555 560

Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser
565 570 575

Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys
580 585 590

Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser
595 600 605

Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg
610 615 620

Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile
625 630 635 640

Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile
645 650 655

Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly
660 665 670

Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Lys
675 680 685

Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu
690 695 700

Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val
705 710 715 720

Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met
725 730 735

Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly
740 745 750

Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe
755 760 765

Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser
770 775 780

Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser
785 790 795 800

Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser
805 810 815

Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe
820 825 830

Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly
835 840 845

Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala
850 855 860

Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val
865 870 875 880

Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg
885 890 895

Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val
900 905 910

Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro
915 920 925

Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu
930 935 940

Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu
945 950 955 960

Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu
965 970 975

Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn
980 985 990

Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser
995 1000 1005

Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala
1010 1015 1020

Tyr Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln
1025 1030 1035

Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly
1040 1045 1050

Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro
1055 1060 1065

Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met
1070 1075 1080

Pro Thr Phe His Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr
1085 1090 1095

Met Ala Asn Asn Glu Asp Glu Leu Asn Phe Ser Lys Gly Gln Leu
1100 1105 1110

Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu
1115 1120 1125

Thr Asn Gly Leu Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met
1130 1135 1140

Thr Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln
1145 1150 1155

Ala Leu Asp Thr Met Gln Pro Thr Glu Arg Lys Arg Gln Gly Tyr
1160 1165 1170

Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr Met Asp Asp Leu
1175 1180 1185

Gln Leu Phe Glu Gln Lys Thr Leu Leu
1190 1195

<210> 7

<211> 738

<212> DNA

<213> Mus musculus

<400> 7

ccgtcttcca catttccac attgatcgtg tgtacacact ccgaacagac aacatcaacg 60

agaggacggc ctgggtccag aagatcaagg gtgcctcaga gcagtacatc gacactgaga 120

agaagaaaacg ggaaaaggct taccatccc gttctaaaa gacttcaggt attggcgtc 180

tgtatggtgca tgtcattgaa gctacagaat taaaagcctg caaaccaaac gggaaaagta 240

atccatactg tgaagtcaagc atgggctccc aaagctatac caccaggacc ctgcaggaca 300

cactaaaccc caagtggAAC ttcaactgcc agttcttcat caaggatctt taccaggacg 360

ttctgtgtct cactatgttt gacagagacc agttttctcc agatgacttc ttgggtcgta	420
ctgaagttcc agtggcaaaa atccgaacag aacaggaaag caaaggcccc accacccgccc	480
gactactact gcacgaagtc cccactggag aagtctgggt ccgctttgac ctgcaacttt	540
ttgaacaaaa aactctcctt tgagggcctg gggaaagccag aaccagggga gctgccacaca	600
aggctgggtc taaagacaga ttttgctctc ccaggacaga ggagcatcac atggcttcat	660
ccatcaaaca gccacactcg ctggcctgt attttattgc acactaaatt gctagcaatc	720
tatgcaaaca tgatcttt	738

<210> 8
 <211> 186
 <212> PRT
 <213> Mus musculus

<400> 8

Val Phe His Ile Ser His Ile Asp Arg Val Tyr Thr Leu Arg Thr Asp			
1	5	10	15

Asn Ile Asn Glu Arg Thr Ala Trp Val Gln Lys Ile Lys Gly Ala Ser		
20	25	30

Glu Gln Tyr Ile Asp Thr Glu Lys Lys Lys Arg Glu Lys Ala Tyr Gln		
35	40	45

Ala Arg Ser Gln Lys Thr Ser Gly Ile Gly Arg Leu Met Val His Val		
50	55	60

Ile Glu Ala Thr Glu Leu Lys Ala Cys Lys Pro Asn Gly Lys Ser Asn			
65	70	75	80

Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser Tyr Thr Arg Thr		
85	90	95

Leu Gln Asp Thr Leu Asn Pro Lys Trp Asn Phe Asn Cys Gln Phe Phe		
100	105	110

Ile Lys Asp Leu Tyr Gln Asp Val Leu Cys Leu Thr Met Phe Asp Arg		
115	120	125

Asp Gln Phe Ser Pro Asp Asp Phe Leu Gly Arg Thr Glu Val Pro Val		
130	135	140

Ala Lys Ile Arg Thr Glu Gln Glu Ser Lys Gly Pro Thr Thr Arg Arg			
145	150	155	160

Leu Leu Leu His Glu Val Pro Thr Gly Glu Val Trp Val Arg Phe Asp
165 170 175

Leu Gln Leu Phe Glu Gln Lys Thr Leu Leu
180 185

<210> 9
<211> 1078
<212> DNA
<213> Mus musculus

<400> 9
gaattcggca cgagggctga gagaagcgg a ctccgaggac tctgatgctg aagagaagcc 60
tgttaagcag gaggacttcc cgaagattta ggaccaaaga agttaaagac gggtgtggcaat 120
tttaagccca gccagaaagg cttttcagga ggaaccaagt ctttcatgga ctttggcagc 180
tgggagagac acacgaaagg gatcgggcag aagctgctgc agaagatggg ctacgtccct 240
gggcgtggcc tgggaaagaa cgcacagggg atcatcaacc ccatcgaagc caaacagaga 300
aaaggcaagg gagccgtggg ggcctatggc tcggagagga ccactcagtc tctgcaggac 360
ttccccgtgg ccgactcgga agaggaggca gaagaggagt ttcagaagga gctgagccaa 420
tggagggaaag accccagcgg gagcaagaag aagccaaagt actcttacaa gactgtggag 480
gagctgaagg ccaagggcag ggtcagcaag aagctcacag cacctcagaa ggaactgtct 540
caggtcaagg tgatcgacat gacaggccgg gagcagaagg tgtactacag ctacagccaa 600
atcagccaca agcacagcgt gcccgtgaa ggggtgcccatt tgctggcgca gctgcccccc 660
acagccggca aggaagccag gatgccggc tttgcactgc ctgagctgga gcacaacctg 720
cagctgctca ttgagcgcac ggagcaggag atcatccaga gcgaccggca gctccagtat 780
gagcgggaca tggtggtcag cctgtcgcat gagctggaga agacggccga ggttcttgca 840
catgaggagc gtgtcatctc taacctcagc aaggtgctgg ccctggtgga ggaatgtgag 900
cgccgcattgc agccccatgg caccgacccc ctcactctgg atgagtgtgc ccgcatttt 960
gagacactac aggacaagta ttatgaggag taccgcctgg cggaccgcgc agacctcgct 1020
gtggccattg tctacccgct cgtgaaggac tactttaagg attggcaccc ctcgaggg 1078

<210> 10
<211> 309
<212> PRT
<213> Mus musculus

<400> 10

Gly Thr Lys Ser Phe Met Asp Phe Gly Ser Trp Glu Arg His Thr Lys

1

5

10

15

Gly Ile Gly Gln Lys Leu Leu Gln Lys Met Gly Tyr Val Pro Gly Arg
20 25 30

Gly Leu Gly Lys Asn Ala Gln Gly Ile Ile Asn Pro Ile Glu Ala Lys
35 40 45

Gln Arg Lys Gly Lys Gly Ala Val Gly Ala Tyr Gly Ser Glu Arg Thr
50 55 60

Thr Gln Ser Leu Gln Asp Phe Pro Val Ala Asp Ser Glu Glu Ala
65 70 75 80

Glu Glu Glu Phe Gln Lys Glu Leu Ser Gln Trp Arg Lys Asp Pro Ser
85 90 95

Gly Ser Lys Lys Pro Lys Tyr Ser Tyr Lys Thr Val Glu Glu Leu
100 105 110

Lys Ala Lys Gly Arg Val Ser Lys Lys Leu Thr Ala Pro Gln Lys Glu
115 120 125

Leu Ser Gln Val Lys Val Ile Asp Met Thr Gly Arg Glu Gln Lys Val
130 135 140

Tyr Tyr Ser Tyr Ser Gln Ile Ser His Lys His Ser Val Pro Asp Glu
145 150 155 160

Gly Val Pro Leu Leu Ala Gln Leu Pro Pro Thr Ala Gly Lys Glu Ala
165 170 175

Arg Met Pro Gly Phe Ala Leu Pro Glu Leu Glu His Asn Leu Gln Leu
180 185 190

Leu Ile Glu Arg Thr Glu Gln Glu Ile Ile Gln Ser Asp Arg Gln Leu
195 200 205

Gln Tyr Glu Arg Asp Met Val Val Ser Leu Ser His Glu Leu Glu Lys
210 215 220

Thr Ala Glu Val Leu Ala His Glu Glu Arg Val Ile Ser Asn Leu Ser
225 230 235 240

Lys Val Leu Ala Leu Val Glu Glu Cys Glu Arg Arg Met Gln Pro His
245 250 255

Gly Thr Asp Pro Leu Thr Leu Asp Glu Cys Ala Arg Ile Phe Glu Thr
260 265 270

Leu Gln Asp Lys Tyr Tyr Glu Glu Tyr Arg Leu Ala Asp Arg Ala Asp
275 280 285

Leu Ala Val Ala Ile Val Tyr Pro Leu Val Lys Asp Tyr Phe Lys Asp
290 295 300

Trp His Pro Ser Arg
305

<210> 11
<211> 97
<212> DNA
<213> Mus musculus

<400> 11
catggcggcg gctgcggagg gcgtccggc gacgcgacgg aggacgagcc acctcgagat 60
gatgctgcgg tggagacagc cgaggaagca aaggagc 97

<210> 12
<211> 123
<212> DNA
<213> Mus musculus

<400> 12
cttgagtcta ctgaaaatac cctgcaggaa gctacatcat ccatgtcttt gatgacccaa 60
tttgaacagg aagtatctgg cctccaaaga ccatacgtga tattgagact agcgaagaga 120
tgc 123

<210> 13
<211> 140
<212> DNA
<213> Mus musculus

<400> 13
gaattcggca cgagggagtc tggttctgga aagccgacag aagctgagct tgtcaactta 60
gatttottgg gagatttggc tgttccggta tctgccccac ccctgtgtgt ctgagctcga 120
gtctctctgc tggactatgg 140

<210> 14
<211> 2855
<212> DNA
<213> Mus musculus

<400> 14

ctttacgagc agagggagcc aaattcagag ccgtttaga taaagctgtg caagcggatg	60
gacaggtgaa ggagcgctac cagtcccatc gagacaccat cgcaattctg tgtaagccgg	120
agccagagct gaatgctgcc atcccctctg ctaacccagc aaagaccatg cagggcagcg	180
aggttgtaag tgtcttaaag tccttattat caaatcttga tgaatcaag aaggaaagag	240
agagtcttga gaatgacctg aagtcagtga attttgacat gacaagcaag ttttgacag	300
ctctggccca agatggcgtg ataaatgagg aggctctctc tgtcaactgag ctggatcgga	360
tctatggcgg tctaacaagt aaagttcaag agtctctgaa gaaacaagag ggacttctaa	420
aaaatataca ggtctcacac caagaattct cccaaatgaa gcaatctaac aacgaggcta	480
acttgagaga agaagttctg aagaacctag caactgcgt a tgacaacttt gttgagcttg	540
tagctaactt gaaggagggc acaaagttt acaatgagct gactgagatc ctggtcaggt	600
tccagaacaa atgcagtgac atagtgttg cacggaagac agaaagagac gagctcttga	660
aggatctgca gcagagcatt gccagagagc ccagcgctcc ttcaatccct cctccagcct	720
atcagtcctc cccagcagcg gggcatgcag cagcgccctc aactccagcc ccaagaacca	780
tgccgcctgc taagccccag cctccagccc gcctccacc tcctgtgctt cctgcaaacc	840
gagttcctcc tgcttctgct gctgctgccc ctgcaggcgt gggacggct tcagcagcgc	900
cgccacagac ccctggctct gtcctccgc cacaggctca gggaccacca taccctacct	960
atccaggata tcccggtat tgccaaatgc ccatgcccatt gggctacaac ccctacgcat	1020
atggccagta caatatgccg taccaccgg tgtatcacca gagccccgga caggctccat	1080
acccaggacc ccagcagcct acctaccct tccctcagcc cccgcagcag tcctactatc	1140
cacagcagta acgctgccac gtgctgctgg ttcagatcag agcgacagga cagcagctgc	1200
caccagctct aagccacgct ctggccactc gagagtatct tgctctattt attgctgtgg	1260
atgatttctg tctgtggcta aagccgaagg ctggggccca cctccacatt tgatcgact	1320
cgtgagattc tgctgctgtt gcagtataaa cgctagctat aatagcattt gaaaaaaaaatt	1380
acagttccat aaaatgctga aaatgagaaa ttaaacctgc aagtgaaaca tttgaaattt	1440
gcataactta taagatgcag ttgggacaaa gatggctaa gtactgatatt ttaaggaaaa	1500
agttttcttt ctcttttgtt ttattgattt agtttaattt ctattatgat attttgcata	1560
atcaaggcat tgtaaatctt ataattaaa aataaattac ttacgaacag ttgtcattgt	1620
tatgtttgtt cattgattct cattgctgtc tagttccctt ctggatttag cctctccctc	1680
tgtatgtca caggctccat tactgtgttg aattgcgtga cgtcaggtga gcagtcagg	1740
agggctgctc tgccggacgcc aagcgcacac cagcttgctc caggctcagc agtcagctca	1800
tctggacatt tctatttaaa agtcctttaa tgtggaagat acacacaatt gttaccaaag	1860

gttcttccaa ttaattttac aatttaaaaa gtatgtatta atgtttattt gttagattt	1920
ccaaaaaaaaat gatgcaaatt ctggtaatat tcatttcctt caccataat ttggtaaaa	1980
tgagtagttt tagccataca gtctcatctg ctgtggagga acctggagaa agtcccctgt	2040
gcctttctag cccttgggtt ctattctt cctgcaatgt ctactgcaca gtgtgtttga	2100
gcagatccta accctcctt tacagttct tcttcttact tcttattct ttttggct	2160
cctgaaatct gaggttattt tgtaattcag gagcatgcag gacaattgtt gggacatgtg	2220
cctagtcgg aatacagccc aggacagcaa ggagatgcgt cctgcaccag gaagccgtgc	2280
aggcaggagc tgtccaagg cccggcggct ctgcctgtgt gaggcaggag aatgagcaga	2340
ttccctaatac tatgttctcg aagttaatg ctgatgttgt ctgccttat cctcattaa	2400
ctgatactgt cacccagtcc accttgctc tcattgcaaa gtgatagtgt aattcaaat	2460
gtaagactga agatacgtt gtaaaaggga gtaaaactgggt ttaaacgtgt tattctaaag	2520
caccttactt tggtgttgc tgcagaaaac acagatgcgc taattcagta taaatgactg	2580
attgccttggaa atttggacgt tggcttaag tccgatagct aaaccttggc aaaacataac	2640
aaacatttca ttgctcagcc tcagtgtctt ggagtattca gtgtatgaga caggttatt	2700
tgagtctctt gtaaaatggca tttgaatttt atattctccc ctcccgagta tcttataaga	2760
catccctga gtttagggagt tcccagactg ctactctatt ccttatgaat gcaaaacaac	2820
caccaataga aaaaaaaaaa aaaaaaaaaac tcgag	2855

<210> 15
 <211> 1151
 <212> DNA
 <213> Mus musculus

<400> 15	
ctttacgagc agagggagcc aaattcagag ccgtttttaga taaagctgtg caagcggatg	60
gacaggtgaa ggagcgctac cagtccttccatc gagacaccat cgcaattctg tgtaagccgg	120
agccagagct gaatgctgcc atccctctg ctaacccagc aaagaccatg cagggcagcg	180
aggttgtaag tgtcttaag tccttattat caaatcttga tgaaatcaag aaggaaagag	240
agagtcttga gaatgacctg aagtcaatgtca attttgcacat gacaagcaag ttttgacag	300
ctctggccca agatggcggtg ataaatgagg aggctcttc tgcactgag ctggatcgga	360
tctatggcggtg tctaacaagt aaagttcaag agtctcttgc gaaacaagag ggacttctaa	420
aaaatataca ggtctcacac caagaattctt cccaaatgaa gcaatctaac aacgaggcta	480
acttgagaga agaagttctg aagaacctag caactgcgtt tgacaacttt gttgagcttg	540
tagctaactt gaaggagggc acaaagttt acaatgagct gactgagatc ctggtcaggt	600

tccagaacaa atgcagtgcac atagtgttg cacggaagac agaaagagac gagctttga	660
aggatctgca gcagagcatt gccagagagc ccagcgctcc ttcaatccct cctccagcct	720
atcagtcctc cccagcagcg gggcatgcag cagcgcctcc aactccagcc ccaagaacca	780
tgccgcctgc taagccccag cctccagccc gcgcctccacc tcctgtgctt cctgcaaacc	840
gagttcctcc tgcttctgtc gctgctgccc ctgcaggcgt ggggacggct tcagcagcgc	900
cgccacagac ccctggctct gctccccgc cacaggctca gggaccacca taccctacct	960
atccaggata tccccggtat tgccaaatgc ccatgccat gggctacaac ccctacgcat	1020
atggccagta caatatgccg taccaccgg tgtatcacca gagccccgga caggctccat	1080
acccaggacc ccagcagcct acctaccct tccctcagcc cccgcagcag tcctactatc	1140
cacagcagta a	1151

<210> 16
 <211> 382
 <212> PRT
 <213> Mus musculus

<400> 16

Leu Arg Ala Glu Gly Ala Lys Phe Arg Ala Val Leu Asp Lys Ala Val			
1	5	10	15
10	15		

Gln Ala Asp Gly Gln Val Lys Glu Arg Tyr Gln Ser His Arg Asp Thr			
20	25	30	
30			

Ile Ala Leu Leu Cys Lys Pro Glu Pro Glu Leu Asn Ala Ala Ile Pro			
35	40	45	
45			

Ser Ala Asn Pro Ala Lys Thr Met Gln Gly Ser Glu Val Val Ser Val			
50	55	60	
60			

Leu Lys Ser Leu Leu Ser Asn Leu Asp Glu Ile Lys Lys Glu Arg Glu			
65	70	75	80
75	80		

Ser Leu Glu Asn Asp Leu Lys Ser Val Asn Phe Asp Met Thr Ser Lys			
85	90	95	
95			

Phe Leu Thr Ala Leu Ala Gln Asp Gly Val Ile Asn Glu Glu Ala Leu			
100	105	110	
110			

Ser Val Thr Glu Leu Asp Arg Ile Tyr Gly Gly Leu Thr Ser Lys Val			
115	120	125	
125			

Gln Glu Ser Leu Lys Lys Gln Glu Gly Leu Leu Lys Asn Ile Gln Val
130 135 140

Ser His Gln Glu Phe Ser Lys Met Lys Gln Ser Asn Asn Glu Ala Asn
145 150 155 160

Leu Arg Glu Glu Val Leu Lys Asn Leu Ala Thr Ala Tyr Asp Asn Phe
165 170 175

Val Glu Leu Val Ala Asn Leu Lys Glu Gly Thr Lys Phe Tyr Asn Glu
180 185 190

Leu Thr Glu Ile Leu Val Arg Phe Gln Asn Lys Cys Ser Asp Ile Val
195 200 205

Phe Ala Arg Lys Thr Glu Arg Asp Glu Leu Leu Lys Asp Leu Gln Gln
210 215 220

Ser Ile Ala Arg Glu Pro Ser Ala Pro Ser Ile Pro Pro Pro Ala Tyr
225 230 235 240

Gln Ser Ser Pro Ala Ala Gly His Ala Ala Ala Pro Pro Thr Pro Ala
245 250 255

Pro Arg Thr Met Pro Pro Ala Lys Pro Gln Pro Pro Ala Arg Pro Pro
260 265 270

Pro Pro Val Leu Pro Ala Asn Arg Val Pro Pro Ala Ser Ala Ala Ala
275 280 285

Ala Pro Ala Gly Val Gly Thr Ala Ser Ala Ala Pro Pro Gln Thr Pro
290 295 300

Gly Ser Ala Pro Pro Gln Ala Gln Gly Pro Pro Tyr Pro Thr Tyr
305 310 315 320

Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro Met Pro Met Gly Tyr Asn
325 330 335

Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro Tyr Pro Pro Val Tyr His
340 345 350

Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly Pro Gln Gln Pro Thr Tyr
355 360 365

Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr Tyr Pro Gln Gln

370

375

380

ctggagaaga	taactgttct	aatagaggat	aatcgaattt	attgtcaagt	ggatgttatt	1620
tattggatag	tgacagagtt	tattttaac	cttaattata	ttaaaagtta	ttctgttagg	1680
atgtttgtt	ttaataaaacg	tgaacaaaat	aaaaaaaaaa	aaaaaaaaaa	ctcgaggg	1738
<210> 18						
<211> 1521						
<212> DNA						
<213> Mus musculus						
<220>						
<221> misc_feature						
<222> (102)..(103)						
<223> "n" represents any nucleotide.						
<400> 18						
gagaaggcgg	cctgccgcag	cgggacaacc	tagagcgcga	cgtggaggcg	cgtagcggag	60
ctggagcaac	tgcgccaccga	ggtggatgtg	cgcattagcg	cnntggacac	ctgcgtcaag	120
gccaagtgcgc	tgccagccgt	cccgccgaga	gtctcaggcc	caccccccga	ccctccaccc	180
attgatccag	ctagcctgga	ggaattcaag	aaaaggatcc	tggagtctca	gcggctccct	240
gtagtcaacc	ctgcwgccca	acccagcggt	tgagracc	gctgccgcag	gacgctgggt	300
gccagaatcg	cccacctgtg	gatgggggca	gccaggtgcc	cacagtgctg	gacacccgccc	360
gtgcctgccc	gcagcctcca	ccccagcgc	cttctctggc	accccttcac	tgtcccstgc	420
atccccrcca	ttcscasws	askggattta	aggcacacac	agctgtgaga	tgacttcaca	480
tcgaccctt	gtgcagtgac	ccggatggtg	ccccacccac	acatgaagca	cccacagctc	540
agctgccacc	ctaggcaact	cctccggttt	cctatca	tgctcctgac	ccgggaggtg	600
agaacaggaa	gcccagcctt	cagctccctt	gggagttcc	agcctccctc	ttaaaggcca	660
ctagggtttc	cagatcctat	ttgagagtct	ccagggctcc	cctgaagggt	tctagccacc	720
acgcccacag	gattcccatt	aggtttaaa	gtctttcca	gagtccgctg	gttcccctcc	780
tcctcacaag	gaagggcctc	aattttagat	gagcgttccg	ggtgatctt	agagccctag	840
agggaggctt	ttgcttgta	ccccctaaag	atattactgg	cacataataa	atatgaaagt	900
ccttgaaag	ttggacactg	cgcaaatggg	gctctccatg	gaccgcagcc	catacggcc	960
cacggggac	cagcagcg	gctctggttc	tacctgcgt	atttcttcct	cttcgtgtcg	1020
ctcattcagt	tcctcatcat	cctgggcctg	gtcctttca	tgtatctatgg	caatgtgcac	1080
gccaccactg	agtccagcct	gccccccacg	gagatccgcg	ccgacagcct	gtacagccag	1140
gtggttggac	tatcgccctc	acaggctaac	ctgagcaa	agctgaacat	cagcttgctt	1200
gtcaaggaaa	cagtcatgca	gcaactgtt	actacgcgac	gtgagatgga	gcccacatcaac	1260

gccagcttcc	gccagtgc	aggcgacctg	atcacctaca	taaactataa	tcgcttc	atc	1320							
gccgctatca	tcctgagc	gaagcagtgc	caggaac	agc	tgaaggaggt	caacaagacc	1380							
tgcgaacttt	actcttcaag	ctgggagaaa	aagttaa	agac	actggagatg	gaggtggcc	1440							
aggagaaggc	agtgtgctcc	aaggacaagg	agagc	c	gcaggaaag	cggcagacgg	1500							
aagagcagct	ggaggc	ctgt	g				1521							
<210> 19														
<211> 720														
<212> DNA														
<213> Mus musculus														
<400> 19														
tgtgc	ccgc	ctctaga	act	agtggat	ccc	ccgggc	ctgc	aggaatt	ccg	gcacg	acggc	60		
cgagc	ccgc	ggaccac	cccg	cggctg	cccg	ccgagcc	gtc	gacatgt	ggg	ggact	gggg	120		
tgggagc	gggc	cggagc	agcg	ccaggta	ccc	gggcgc	cg	aaccatgg	ctcg	ctcg	cc	180		
tgtc	cctg	acc	tggctt	gctc	gccc	cacc	accg	agaatgt	tcag	cca	gggaa	ccct	240	
cctc	gtc	c	cgc	cgag	ggacc	ccgg	cag	ccctc	caa	aacc	atgg	accc	300	
tca	agat	cat	agtgg	aggat	ctgg	aaatt	ag	tc	c	ct	ggagg	ac	360	
aact	taa	agga	gggt	ttgac	cagatt	gaca	cc	ctg	gac	t	tg	ggcc	aa	420
agat	gacc	ga	cag	ctcc	aa	ac	agac	actc	tga	ac	ac	agc	ct	480
ccag	cat	aga	ga	atg	ccct	cc	atg	ccct	cat	aa	cc	cc	cc	540
cgt	tctg	ctat	cctg	actgt	gtc	ctg	aga	aa	acc	cc	cc	cc	cc	600
cacc	cg	tg	gt	gt	ga	tg	gt	cc	ac	cc	cc	cc	cc	660
atgg	cact	ct	tct	gc	gg	agg	ctt	g	gg	gg	gg	gg	gg	720
<210> 20														
<211> 801														
<212> DNA														
<213> Mus musculus														
<400> 20														
ctcgag	tttt	tttttttt	tttttttt	ttt	cattatt	tactattt	tatt	tgacata					60	
ttt	ccaa	agc	tca	aaat	att	ttaca	tat	gtgaa	cat	atgtt	tc	aaattgt	tata	120
gtat	aga	aaa	aaact	tttt	tgt	atgtgt	cc	tca	tc	atgt	ca	aaactt	gac	180
aaat	ctt	taa	act	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	240
tagat	caa	ag	gg	gaga	actat	gacat	cat	atg	cat	atg	atg	atg	atg	300
gagtt	gc	cc	ct	gg	ttt	tat	ca	aca	at	at	ct	cc	ag	360
caaaata	actt	g	gaat	cag	aa	gtc	ac	ag	tt	at	gg	at	ca	420

tcattcatac ttctcaatt ttccgcagtt tctgatgatg gaacatagaa aacaatgtac	480
gtccaggaca gaggcgctac tctgcatact taccacgtga tttttatgc cactttgttgc	540
aatgcagatt aatatatttg ggcttttat tgcttgagta gaaagtgcctc attacttattt	600
atttacgtt tatcatatag aaaataaaaa acaaacagaa cgtttctta aatggcagat	660
atcacactgt ggttgtggtg gatccctca ggatggtctt ctgtggtttt ggtgcagcgg	720
gaggaggcac ggtgcaggt gtgggagggg ggaaactgtt actgtggctt attcccagtc	780
ccccatttc taatggaaa t	801
<210> 21	
<211> 119	
<212> DNA	
<213> Mus musculus	
<400> 21	
gcacagcccc cctccatcct gaagaaaacc tcagcgtatg ggctccagc ttcggccgt	60
gtctatcctt cctctcctgg gacatggtgt tccccgctt ccccccctggc agaaaaccg	119
<210> 22	
<211> 5738	
<212> DNA	
<213> Mus musculus	
<400> 22	
cggcacgagg aggagtggag cggcgcgaaa agggcgcgca gcttggttgc tccgtagttac	60
ggcggctcgc aaggagcat cccgagcggg ctccgggacg gccgggagggc aggcaggcgg	120
gcgggcgggg atgggtgtcg cggctgcggc ctccgggttc ctgcgcggc gtgcgggctg	180
cactgatttgc tgtgaggggc ggcgcgcgc acccgcccg agatgaggcg tcgatcagca	240
aggtgaacgt aatagaacca tggctcagtt tcccacacct ttccgtggta gcctggatgt	300
ctggccata actgtggagg aaaggccaa gcatgaccag cagttcctta gcctgaagcc	360
gatagcggga ttttattactg gtgatcaagc gagaaacttt ttttccat ctgggttacc	420
tcagcctgtc ttagcacaaa tatggcgct agcggacatg aataacgtatg gaaggatggaa	480
tcaagtggaa ttttccatag ccatgaagct tatcaaactg aagctacaag gatatcagct	540
ccctccaca cttccccctg tcatgaaaca gcaaccagtg gctatttcca gtgcaccagc	600
atttggata ggagggattt ctagcatgcc accactcaca gctgttgcctc ctgtgccaat	660
gggctccatt ccagttgttg gaatgtctcc acccttagta tcttctgtcc ctccagcagc	720
agtgcctccc ctggctaacg gggctccctcc cgtcatacag cctctgcctg cgtttgcgc	780
tcctgcagcc acatggccaa agagttcttc cttcagcaga tctggtccag ggtcacaatt	840

aaacactaag ttacagaagg cacaatcatt cgatgtcgcc agcgccctc cagcagcaga	900
atgggctgtg cctcagtcat caaggctgaa atacaggcag ttattcaaca gccacgacaa	960
aactatgagt ggacacttaa caggtccccca ggcaagaact attctcatgc aatcaagttt	1020
accccaggct cagctggctt caatatggaa tctttctgac attgatcaag atggaaaact	1080
cactgcagaa gaatttatcc tagctatgca cctaattgat gttgccatgt ctggtcagcc	1140
actgccgccc gtcctgcctc cagaatacat ccctccttcc ttcagaagag ttcgctccgg	1200
cagtggatg tccgtcataa gctcttcttc tgtggatcag aggctgcctg aggagccgtc	1260
gtcagaggat gaggcagc cagagaagaa actgcctgtg acatttgaag ataagaagcg	1320
ggagaacttc gagcgaggca gtgtggagct ggagaagcgc cggcaagcgc tcttggagca	1380
gcagcgc当地 gagcaggagc ggttggctca gctggagcgc gccgagcagg agagggaaaga	1440
gcgggagcgc caggagcagg aggccaagcg gcagctggag ctggagaagc agctggagaa	1500
gcagcgggag ctggagcggc agcgagagga ggagaggagg aaggagatcg agaggcgc当地	1560
ggccgc当地 cgggaactgg aaaggcagcg acaacttcaa tgggaacgga accggagaca	1620
ggaactcctg aatcagagga acaaggagca ggagggcacc gtggcctga aggcaaggag	1680
gaagactctg gagtttgagt tagaagctct gaatgacaaa aagcatcagc tagaaggaaa	1740
acttcaggat atcaggtgtc gactggcaac ccagaggcaaa gaaattgaga gcacgaacaa	1800
gtctagagag ctaagaatttgc当地 ctgaaatcac ccacttacag cagcagttgc aggaatctca	1860
gcaaattgtt ggaagactta ttccagagaa acagatactc agtgaccagt taaaacaagt	1920
ccagcagaac agtttgc当地 gagactcgct tcttaccctc aaaagagcct tggaagcaaa	1980
ggagctggcc cggcagcagc tccggagca gctggacgag gtggagagag agaccaggc当地	2040
aaagctgc当地 gagattgatg tttcaacaa ccagctgaag gaactgagag agatacatag	2100
caaacagcaa ctccagaagc agaggtccct ggaggcagcg cgactgaagc agaaagagca	2160
ggagaggaag agcctggagc tagagaagca aaaggaagac gctcagagac gagttcagga	2220
aagggacaag caatggctgg agcatgtgca gcaggaggag cagccacgcc cccggaaacc	2280
ccacgaggag gacagactga agagggaga cagtgtcagg aagaaggagg cggaaagagag	2340
agccaagccg gaaatgcaag acaagcagag tcggctttc catccgc当地 aggagccagc	2400
taagctggcc acccaggcac cctggtctac cacagagaaa ggcccgctta ccatttctgc	2460
acaggagagt gtaaaagtgg tatattaccg agcgctgtac cccttgaat ccagaagtca	2520
cgtgagatc accatccagc caggagatat agtcatgtg gatgaaagcc agactggaga	2580
gccaggatgg cttggaggag agctgaaagg gaagacggga tggccctg ccaaactatgc	2640
agaaaaagatt ccagaaaatg aggtcccac tccagccaaa ccagtgaccg atctgacatc	2700

tgccccgtcc cccaaactgg ctctgcgtga gaccctgtct ccttgccag tgacctttc	2760
tgagccctcc acaaccccca acaactgggc agacttcagt tccacgtggc ccagcagctc	2820
aaacgagaag ccagaaacgg acaactggga tacgtggcg gctcagcett ctctgaccgt	2880
acctagtgtct ggccagttac ggcagagatc agccttacc ccagccacag ccactggctc	2940
ctccccatct cccgtcctgg gccagggtga aaaggtggaa gggctacaag cgcaaggccct	3000
gtatccctgg agagccaaa aagacaacca cttaaatttt aacaaaagtg acgtcatcac	3060
cgttctggaa cagcaagaca tgtggtggtt tggagaagtt caaggtcaga agggttggtt	3120
ccccaaagtct tacgtgaaac tcatttcagg gcccgtaagg aaatccacaa gcatcgatac	3180
tggccctact gaaagtccctg ctagtctaaa gagagtggct tccccggccg ccaagccagc	3240
cattcccgga gaagagtttta ttgccatgtac cacatacgag agttctgagc aaggagattt	3300
aaccttcag caaggggatg tgattgttgtt taccaagaaa gatggtgact ggtggacggg	3360
aacgggtggc gacaagtccg gagtcttccc ttcttaactat gtgaggctta aagattcaga	3420
gggctctgga actgctggga aaacagggag ttttagaaaa aaacctgaaa ttgcccaggt	3480
tattgcttcc tacgctgcta ctggtcccga acaactcacc ctggctcctg ggcagctgat	3540
tctgatccgg aaaaagaacc caggtggatg gtgggaagga gaactgcaag ctcgagggaa	3600
aaagcgccag atagggtggt ttccagcaaa ttatgtcaaa cttctaagcc ccggaacaag	3660
caaaatcacc ccaactgagc taccgaagac cgcagtgcag ccagcagtgt gccaggtgat	3720
cgggatgtac gattacaccg cccagaacga tgacgaacta gccttcagca aaggccagat	3780
catcaacgtc ctcaacaagg aggaccggc ctggtgaaaa ggagaagtca gtggcaagt	3840
tgggcttttc ccatccaatt atgtaaagct gaccacagac atggacccca gccagcaatg	3900
gtgctcagac ctgcatactct tagatatgtct gaccccgact gagaggaagc ggcaaggcta	3960
catccatgaa ctcattgtca cggaggagaa ctacgtgaac gacttgcagc tggtcacaga	4020
gatcttcag aaacccctga cggagtctga gctgctgaca gaaaaagagg ttgctatgtat	4080
ttttgttaac tggaaaggagc tgatcatgtg taatatcaaa ctgctgaaag cgctgagagt	4140
ccgcaagaag atgtctgggg agaagatgcc ggtgaagatg attggcgaca tcctgagcgc	4200
ccagctggcg cacatgcagc cttacatccg cttctgcagc tgccagctca atggggctgc	4260
cctcatccag cagaagacgg acgaggctcc agacttcaag gagttcgtca aaagactggc	4320
aatggaccct cggtgcaaag gaatgcctct gtccagcttt atactgaagc ctatgcagcg	4380
tgtcacaaga taccgcgtga tcattaaaaa catcctggaa aacactcctg agaaccatcc	4440
agaccacagc cacctgaagc atgcctggaa aaaggcggag gagctgtgct cccaggtgaa	4500

cgagggagtt cgagagaagg agaactcaga ccggctggag tggatccaag cccacgtgca 4560
 gtgtgaaggc ctttctgagc aactggtgtt caattcagtg accaactgct tgggaccacg 4620
 caagtttctg cacagcggga agctctacaa ggccaagagc aataaagaac tgtatggctt 4680
 cctcttcaac gacttcctcc tgctgaccca aatcacaaag cccttaggct cttccggcac 4740
 cgacaaagtc ttcagcccc aatctaacct tcagtataaa atgtacaaaa cgcgcatttt 4800
 cttaaatgag gttctagtaa aattgcccac ggacccttct ggagatgagc ctatcttcca 4860
 catttcccac atcgaccggg tctacaccct ccgagcagag agcataaatg agaggactgc 4920
 ctgggtgcag aaaatcaagg cggcgtctga gctctacata gagacggaga aaaagaagcg 4980
 agagaaggcg tacctggtcc gttcccagcg ggcgaccggt attggaaggt tcatgggtgaa 5040
 cgtggtagaa ggcattgagc tgaagccctg tcggtcacat ggaaagagca acccgtaactg 5100
 tgaggtgacc atgggctctc agtgcacat caccaagaca atccaggaca cgctaaaccc 5160
 caagtggaat tctaactgcc agttctcat cagagacctg gagcaggagg ttctctgcat 5220
 cacagtgttt gagagggacc agttctgcc tcatggattt ttgggtcgga cagagatccg 5280
 agtggccgac atcaagaaag accagggctc caagggccg gttacgaagt gtctctgct 5340
 gcatgaggtc cccacgggag agattgtggt ccgccttgac ctgcagttgt ttgatgagcc 5400
 gtagcagccc tgcgatgatc gtagatgact tcctcctcaa ggccccgtgc gggcgtgctg 5460
 tctggggtc agcctcagag caacggggat gaagcaaaga cgaagccct cgaggctgct 5520
 aggagtcgtt ctgcacaatc ctgccttca aaccatgtct cattttatga atccaaattc 5580
 tctttccct tgctctccct atggctcat catggcttct agagtctctg aaatctgtga 5640
 ccttaacta ggttccattt ggagcctggc tcctccctg ggctggaggt gtgggtctgg 5700
 tttctataaa atagattata aactcgagaa tcactagt 5738

<210> 23
 <211> 5145
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(5145)
 <223> Mouse Esell

<400> 23
 atg gct cag ttt ccc aca cct ttc ggt ggt agc ctg gat gtc tgg gcc 48
 Met Ala Gln Phe Pro Thr Pro Phe Gly Gly Ser Leu Asp Val Trp Ala
 1 5 10 15

ata act gtg gag gaa agg gcc aag cat gac cag cag ttc ctt agc ctg 96
 Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu

20	25	30	
aag ccg ata gcg gga ttt att act ggt gat caa gcg agg aac ttt ttt Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe 35	40	45	144
ttc caa tct ggg tta cct cag cct gtc tta gca caa ata tgg gcg cta Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu 50	55	60	192
gcg gac atg aat aac gat gga agg atg gat caa gtg gaa ttt tcc ata Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile 65	70	75	240
gcc atg aag ctt atc aaa ctg aag cta caa gga tat cag ctc ccc tcc Ala Met Lys Leu Ile Lys Leu Lys Gln Gly Tyr Gln Leu Pro Ser 85	90	95	288
aca ctt ccc cct gtc atg aaa cag caa cca gtg gct att tcc agt gca Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala 100	105	110	336
cca gca ttt ggt ata gga ggg att gct agc atg cca cca ctc aca gct Pro Ala Phe Gly Ile Gly Ile Ala Ser Met Pro Pro Leu Thr Ala 115	120	125	384
gtt gct cct gtg cca atg ggc tcc att cca gtt gtt gga atg tct cca Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro 130	135	140	432
ccc tta gta tct tct gtc cct cca gca gca gtg cct ccc ctg gct aac Pro Leu Val Ser Ser Val Pro Pro Ala Ala Val Pro Pro Leu Ala Asn 145	150	155	480
ggg gct cct ccc gtc ata cag cct ctg cct gcg ttt gcg cat cct gca Gly Ala Pro Pro Val Ile Gln Pro Leu Pro Ala Phe Ala His Pro Ala 165	170	175	528
gcc aca tgg cca aag agt tct tcc ttc agc aga tct ggt cca ggg tca Ala Thr Trp Pro Lys Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser 180	185	190	576
caa tta aac act aag tta cag aag gca caa tca ttc gat gtc gcc agc Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser 195	200	205	624
gcc cct cca gca gca gaa tgg gct gtg cct cag tca tca agg ctg aaa Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys 210	215	220	672
tac agg cag tta ttc aac agc cac gac aaa act atg agt gga cac tta Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu 225	230	235	720
aca ggt ccc cag gca aga act att ctc atg caa tca agt tta ccc cag Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln 245	250	255	768
gct cag ctg gct tca ata tgg aat ctt tct gac att gat caa gat gga Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly 260	265	270	816

aaa ctc act gca gaa gaa ttt atc cta gct atg cac cta att gat gtt Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val 275 280 285	864
gcc atg tct ggt cag cca ctg ccg ccc gtc ctg cct cca gaa tac atc Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile 290 295 300	912
cct cct tcc ttc aga aga gtt cgc tcc ggc agt ggg atg tcc gtc ata Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile 305 310 315 320	960
agc tct tct gtg gat cag agg ctg cct gag gag ccg tcg tca gag Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu 325 330 335	1008
gat gag cag cag cca gag aag aaa ctg cct gtg aca ttt gaa gat aag Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys 340 345 350	1056
aag cgg gag aac ttc gag cga ggc agt gtg gag ctg gag aag cgc cgg Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg 355 360 365	1104
caa gcg ctc ttg gag cag cag cgc aaa gag cag gag cgg ttg gct cag Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln 370 375 380	1152
ctg gag cgc gcc gag cag gag agg aaa gag cgg gag cgc cag gag cag Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln 385 390 395 400	1200
gag gcc aag cgg cag ctg gag aag cag ctg gag aag cag cgg Glu Ala Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln Arg 405 410 415	1248
gag ctg gag cgg cag cga gag gag gag agg aag gag atc gag agg Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg 420 425 430	1296
cgc gag gcc gca aaa cgg gaa ctg gaa agg cag cga caa ctt gaa tgg Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp 435 440 445	1344
gaa cgg aac cgg aga cag gaa ctc ctg aat cag agg aac aag gag cag Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln 450 455 460	1392
gag ggc acc gtg gtc ctg aag gca agg agg aag act ctg gag ttt gag Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu 465 470 475 480	1440
tta gaa gct ctg aat gac aaa aag cat cag cta gaa gga aaa ctt cag Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln 485 490 495	1488
gat atc agg tgt cga ctg gca acc cag agg caa gaa att gag agc acg Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr 500 505 510	1536

aac aag tct aga gag cta aga att gct gaa atc acc cac tta cag cag Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln 515 520 525	1584
cag ttg cag gaa tct cag caa atg ctt gga aga ctt att cca gag aaa Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys 530 535 540	1632
cag ata ctc agt gac cag tta aaa caa gtc cag cag aac agt ttg cat Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His 545 550 555 560	1680
aga gac tcg ctt ctt acc ctc aaa aga gcc ttg gaa gca aag gag ctg Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu 565 570 575	1728
gcc cgg cag cag ctc cgg gag cag ctg gac gag gtg gag aga gag acc Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr 580 585 590	1776
agg tca aag ctg cag gag att gat gtt ttc aac aac cag ctg aag gaa Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu 595 600 605	1824
ctg aga gag ata cat agc aaa cag caa ctc cag aag cag agg tcc ctg Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu 610 615 620	1872
gag gca gcg cga ctg aag cag aaa gag cag gag agg aag agc ctg gag Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu 625 630 635 640	1920
tta gag aag caa aag gaa gac gct cag aga cga gtt cag gaa agg gac Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp 645 650 655	1968
aag caa tgg ctg gag cat gtg cag cag gag cag cca cgc ccc cgg Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg 660 665 670	2016
aaa ccc cac gag gag gac aga ctg aag agg gaa gac agt gtc agg aag Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys 675 680 685	2064
aag gag gcg gaa gag aga gcc aag ccg gaa atg caa gac aag cag agt Lys Glu Ala Glu Glu Arg Ala Lys Pro Glu Met Gln Asp Lys Gln Ser 690 695 700	2112
cgg ctt ttc cat ccg cat cag gag cca gct aag ctg gcc acc cag gca Arg Leu Phe His Pro His Gln Glu Pro Ala Lys Leu Ala Thr Gln Ala 705 710 715 720	2160
ccc tgg tct acc aca gag aaa ggc ccg ctt acc att tct gca cag gag Pro Trp Ser Thr Thr Glu Lys Gly Pro Leu Thr Ile Ser Ala Gln Glu 725 730 735	2208
agt gta aaa gtg gta tat tac cga gcg ctg tac ccc ttt gaa tcc aga Ser Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg 740 745 750	2256
agt cac gat gag atc acc atc cag cca gga gat ata gtc atg gtg gat	2304

Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp			
755	760	765	
gaa agc cag act gga gag cca gga tgg ctt gga gga gag ctg aaa ggg			2352
Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly			
770	775	780	
aag acg gga tgg ttc cct gca aac tat gca gaa aag att cca gaa aat			2400
Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro Glu Asn			
785	790	795	800
gag gtt ccc act cca gcc aaa cca gtg acc gat ctg aca tct gcc cct			2448
Glu Val Pro Thr Pro Ala Lys Pro Val Thr Asp Leu Thr Ser Ala Pro			
805	810	815	
gcc ccc aaa ctg gct ctg cgt gag acc cct gct ttg cca gtg acc			2496
Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Pro Val Thr			
820	825	830	
tct tct gag ccc tcc aca acc ccc aac aac tgg gca gac ttc agt tcc			2544
Ser Ser Glu Pro Ser Thr Pro Asn Asn Trp Ala Asp Phe Ser Ser			
835	840	845	
acg tgg ccc agc agc tca aac gag aag cca gaa acg gac aac tgg gat			2592
Thr Trp Pro Ser Ser Asn Glu Lys Pro Glu Thr Asp Asn Trp Asp			
850	855	860	
acg tgg gcg gct cag cct tct ctg acc gta cct agt gct ggc cag tta			2640
Thr Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly Gln Leu			
865	870	875	880
cgg cag aga tca gcc ttt acc cca gcc aca gcc act ggc tcc tcc cca			2688
Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser Ser Pro			
885	890	895	
tct ccc gtc ctg ggc cag ggt gaa aag gtg gaa ggg cta caa gcg caa			2736
Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln Ala Gln			
900	905	910	
gcc ctg tat ccc tgg aga gcc aaa aaa gac aac cac tta aat ttt aac			2784
Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn Phe Asn			
915	920	925	
aaa agt gac gtc atc acc gtt ctg gaa cag caa gac atg tgg tgg ttt			2832
Lys Ser Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp Trp Phe			
930	935	940	
gga gaa gtt caa ggt cag aag ggt tgg ttc ccc aag tct tac gtg aaa			2880
Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr Val Lys			
945	950	955	960
ctc att tca ggg ccc gta agg aaa tcc aca agc atc gat act ggc cct			2928
Leu Ile Ser Gly Pro Val Arg Lys Ser Thr Ser Ile Asp Thr Gly Pro			
965	970	975	
act gaa agt cct gct agt cta aag aga gtg gct tcc ccg gcc gcc aag			2976
Thr Glu Ser Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala Ala Lys			
980	985	990	
cca gcc att ccc gga gaa gag ttt att gcc atg tac aca tac gag agt			3024
Pro Ala Ile Pro Gly Glu Glu Phe Ile Ala Met Tyr Thr Tyr Glu Ser			

995	1000	1005	
tct gag caa gga gat tta acc	ttt cag caa ggg gat	gtg att gtg	3069
Ser Glu Gln Gly Asp Leu Thr	Phe Gln Gln Gly Asp	Val Ile Val	
1010	1015	1020	
gtt acc aag aaa gat ggt gac	tgg tgg acg gga acg	gtg ggc gac	3114
Val Thr Lys Lys Asp Gly Asp	Trp Trp Thr Gly Thr	Val Gly Asp	
1025	1030	1035	
aag tcc gga gtc ttc cct tct	aac tat gtg agg ctt	aaa gat tca	3159
Lys Ser Gly Val Phe Pro Ser	Asn Tyr Val Arg Leu	Lys Asp Ser	
1040	1045	1050	
gag ggc tct gga act gct ggg	aaa aca ggg agt tta	gga aaa aaa	3204
Glu Gly Ser Gly Thr Ala Gly	Lys Thr Gly Ser Leu	Gly Lys Lys	
1055	1060	1065	
cct gaa att gcc cag gtt att	gct tcc tac gct gct	act ggt ccc	3249
Pro Glu Ile Ala Gln Val Ile	Ala Ser Tyr Ala Ala	Thr Gly Pro	
1070	1075	1080	
gaa caa ctc acc ctg gct cct	ggg cag ctg att ctg	atc cgg aaa	3294
Glu Gln Leu Thr Leu Ala Pro	Gly Gln Leu Ile Leu	Ile Arg Lys	
1085	1090	1095	
aag aac cca ggt gga tgg tgg	gaa gga gaa ctg caa	gct cga ggg	3339
Lys Asn Pro Gly Gly Trp Trp	Glu Gly Glu Leu Gln	Ala Arg Gly	
1100	1105	1110	
aaa aag cgc cag ata ggg tgg	ttt cca gca aat tat	gtc aaa ctt	3384
Lys Lys Arg Gln Ile Gly Trp	Phe Pro Ala Asn Tyr	Val Lys Leu	
1115	1120	1125	
cta agc ccc gga aca agc aaa	atc acc cca act gag	cta ccc aag	3429
Leu Ser Pro Gly Thr Ser Lys	Ile Thr Pro Thr Glu	Leu Pro Lys	
1130	1135	1140	
acc gca gtg cag cca gca gtg	tgc cag gtg atc ggg	atg tac gat	3474
Thr Ala Val Gln Pro Ala Val	Cys Gln Val Ile Gly	Met Tyr Asp	
1145	1150	1155	
tac acc gcc cag aac gat gac	gaa cta gcc ttc agc	aaa ggc cag	3519
Tyr Thr Ala Gln Asn Asp Asp	Glu Leu Ala Phe Ser	Lys Gly Gln	
1160	1165	1170	
atc atc aac gtc ctc aac aag	gag gac ccg gac tgg	tgg aaa gga	3564
Ile Ile Asn Val Leu Asn Lys	Glu Asp Pro Asp Trp	Trp Lys Gly	
1175	1180	1185	
gaa gtc agt ggg caa gtt ggg	ctc ttc cca tcc aat	tat gta aag	3609
Glu Val Ser Gly Gln Val Gly	Leu Phe Pro Ser Asn	Tyr Val Lys	
1190	1195	1200	
ctg acc aca gac atg gac ccc	agc cag caa tgg tgc	tca gac ctg	3654
Leu Thr Thr Asp Met Asp Pro	Ser Gln Gln Trp Cys	Ser Asp Leu	
1205	1210	1215	
cat ctc tta gat atg ctg acc	ccg act gag agg aag	cgg caa ggc	3699
His Leu Leu Asp Met Leu Thr	Pro Thr Glu Arg Lys	Arg Gln Gly	
1220	1225	1230	

tac	atc	cat	gaa	ctc	att	gtc	acg	gag	gag	aac	tac	gtg	aac	gac	3744
Tyr	Ile	His	Glu	Leu	Ile	Val	Thr	Glu	Glu	Asn	Tyr	Val	Asn	Asp	
1235						1240						1245			
ttg	cag	ctg	gtc	aca	gag	atc	ttt	cag	aaa	ccc	ctg	acg	gag	tct	3789
Leu	Gln	Leu	Val	Thr	Glu	Ile	Phe	Gln	Lys	Pro	Leu	Thr	Glu	Ser	
1250						1255						1260			
gag	ctg	ctg	aca	gaa	aaa	gag	gtt	gct	atg	att	ttt	gtt	aac	tgg	3834
Glu	Leu	Leu	Thr	Glu	Lys	Glu	Val	Ala	Met	Ile	Phe	Val	Asn	Trp	
1265						1270						1275			
aag	gag	ctg	atc	atg	tgt	aat	atc	aaa	ctg	ctg	aaa	gcg	ctg	aga	3879
Lys	Glu	Leu	Ile	Met	Cys	Asn	Ile	Lys	Leu	Leu	Lys	Ala	Leu	Arg	
1280						1285						1290			
gtc	cgc	aag	aag	atg	tct	ggg	gag	aag	atg	ccg	gtg	aag	atg	att	3924
Val	Arg	Lys	Lys	Met	Ser	Gly	Glu	Lys	Met	Pro	Val	Lys	Met	Ile	
1295						1300						1305			
ggc	gac	atc	ctg	agc	gcc	cag	ctg	ccg	cac	atg	cag	cct	tac	atc	3969
Gly	Asp	Ile	Leu	Ser	Ala	Gln	Leu	Pro	His	Met	Gln	Pro	Tyr	Ile	
1310						1315						1320			
cgc	ttc	tgc	agc	tgc	cag	ctc	aat	ggg	gct	gcc	ctc	atc	cag	cag	4014
Arg	Phe	Cys	Ser	Cys	Gln	Leu	Asn	Gly	Ala	Ala	Leu	Ile	Gln	Gln	
1325						1330						1335			
aag	acg	gac	gag	gct	cca	gac	ttc	aag	gag	ttc	gtc	aaa	aga	ctg	4059
Lys	Thr	Asp	Glu	Ala	Pro	Asp	Phe	Lys	Glu	Phe	Val	Lys	Arg	Leu	
1340						1345						1350			
gca	atg	gac	cct	cg	tgc	aaa	gga	atg	cct	ctg	tcc	agc	ttt	ata	4104
Ala	Met	Asp	Pro	Arg	Cys	Lys	Gly	Met	Pro	Leu	Ser	Ser	Phe	Ile	
1355						1360						1365			
ctg	aag	cct	atg	cag	cgt	gtc	aca	aga	tac	ccg	ctg	atc	att	aaa	4149
Leu	Lys	Pro	Met	Gln	Arg	Val	Thr	Arg	Tyr	Pro	Leu	Ile	Ile	Lys	
1370						1375						1380			
aac	atc	ctg	gaa	aac	act	cct	gag	aac	cat	cca	gac	cac	agc	cac	4194
Asn	Ile	Leu	Glu	Asn	Thr	Pro	Glu	Asn	His	Pro	Asp	His	Ser	His	
1385						1390						1395			
ctg	aag	cat	gcc	ctg	gaa	aag	gcg	gag	gag	ctg	tgc	tcc	cag	gtg	4239
Leu	Lys	His	Ala	Leu	Glu	Lys	Ala	Glu	Glu	Leu	Cys	Ser	Gln	Val	
1400						1405						1410			
aac	gag	gga	gtt	cga	gag	aag	gag	aac	tca	gac	cg	ctg	gag	tgg	4284
Asn	Glu	Gly	Val	Arg	Glu	Lys	Glu	Asn	Ser	Asp	Arg	Leu	Glu	Trp	
1415						1420						1425			
atc	caa	gcc	cac	gtg	cag	tgt	gaa	ggc	ctt	tct	gag	caa	ctg	gtg	4329
Ile	Gln	Ala	His	Val	Gln	Cys	Glu	Gly	Leu	Ser	Glu	Gln	Leu	Val	
1430						1435						1440			
ttc	aat	tca	gtg	acc	aac	tgc	ttg	gga	cca	cgc	aag	ttt	ctg	cac	4374
Phe	Asn	Ser	Val	Thr	Asn	Cys	Leu	Gly	Pro	Arg	Lys	Phe	Leu	His	
1445						1450						1455			

agc ggg aag ctc tac aag gcc	aag agc aat aaa gaa	ctg tat ggc	4419
Ser Gly Lys Leu Tyr Lys Ala	Lys Ser Asn Lys Glu	Leu Tyr Gly	
1460	1465	1470	
tcc ctc ttc aac gac ttc ctc	ctg ctg acc caa atc	aca aag ccc	4464
Phe Leu Phe Asn Asp Phe Leu	Leu Leu Thr Gln Ile	Thr Lys Pro	
1475	1480	1485	
tta ggc tct tcc ggc acc gac	aaa gtc ttc agc ccc	aaa tct aac	4509
Leu Gly Ser Ser Gly Thr Asp	Lys Val Phe Ser Pro	Lys Ser Asn	
1490	1495	1500	
ctt cag tat aaa atg tac aaa	acg ccc att ttc tta	aat gag gtt	4554
Leu Gln Tyr Lys Met Tyr Lys	Thr Pro Ile Phe Leu	Asn Glu Val	
1505	1510	1515	
cta gta aaa ttg ccc acg gac	cct tct gga gat gag	cct atc ttc	4599
Leu Val Lys Leu Pro Thr Asp	Pro Ser Gly Asp Glu	Pro Ile Phe	
1520	1525	1530	
cac att tcc cac atc gac cgg	gtc tac acc ctc cga	gca gag agc	4644
His Ile Ser His Ile Asp Arg	Val Tyr Thr Leu Arg	Ala Glu Ser	
1535	1540	1545	
ata aat gag agg act gcc tgg	gtg cag aaa atc aag	gcg gcg tct	4689
Ile Asn Glu Arg Thr Ala Trp	Val Gln Lys Ile Lys	Ala Ala Ser	
1550	1555	1560	
gag ctc tac ata gag acg gag	aaa aag aag cga gag	aag gcg tac	4734
Glu Leu Tyr Ile Glu Thr Glu	Lys Lys Arg Glu	Lys Ala Tyr	
1565	1570	1575	
ctg gtc cgt tcc cag cgg gcg	acc ggt att gga agg	ttg atg gtg	4779
Leu Val Arg Ser Gln Arg Ala	Thr Gly Ile Gly Arg	Leu Met Val	
1580	1585	1590	
aac gtg gta gaa ggc att gag	ctg aag ccc tgt cgg	tca cat gga	4824
Asn Val Val Glu Gly Ile Glu	Leu Lys Pro Cys Arg	Ser His Gly	
1595	1600	1605	
aag agc aac ccg tac tgt gag	gtg acc atg ggc tct	cag tgc cac	4869
Lys Ser Asn Pro Tyr Cys Glu	Val Thr Met Gly Ser	Gln Cys His	
1610	1615	1620	
atc acc aag aca atc cag gac	acg cta aac ccc aag	tgg aat tct	4914
Ile Thr Lys Thr Ile Gln Asp	Thr Leu Asn Pro Lys	Trp Asn Ser	
1625	1630	1635	
aac tgc cag ttc ttc atc aga	gac ctg gag cag gag	gtt ctc tgc	4959
Asn Cys Gln Phe Phe Ile Arg	Asp Leu Glu Gln Glu	Val Leu Cys	
1640	1645	1650	
atc aca gtg ttt gag agg gac	cag ttc tcg cct gat	gat ttt ttg	5004
Ile Thr Val Phe Glu Arg Asp	Gln Phe Ser Pro Asp	Asp Phe Leu	
1655	1660	1665	
ggt cgg aca gag atc cga gtg	gcc gac atc aag aaa	gac cag ggc	5049
Gly Arg Thr Glu Ile Arg Val	Ala Asp Ile Lys Lys	Asp Gln Gly	
1670	1675	1680	
tcc aag ggg ccg gtt acg aag	tgt ctc ctg ctg cat	gag gtc ccc	5094

Ser	Lys	Gly	Pro	Val	Thr	Lys	Cys	Leu	Leu	Leu	His	Glu	Val	Pro	
1685						1690					1695				
acg	gga	gag	att	gtg	gtc	cgc	ctt	gac	ctg	cag	ttg	ttt	gat	gag	5139
Thr	Gly	Glu	Ile	Val	Val	Arg		Leu	Asp	Leu	Gln	Leu	Phe	Asp	Glu
1700							1705					1710			
ccg	tag														5145
Pro															

<210>	24														
<211>	1714														
<212>	PRT														
<213>	Mus musculus														
<400>	24														

Met	Ala	Gln	Phe	Pro	Thr	Pro	Phe	Gly	Gly	Ser	Leu	Asp	Val	Trp	Ala
1										10				15	

Ile	Thr	Val	Glu	Glu	Arg	Ala	Lys	His	Asp	Gln	Gln	Phe	Leu	Ser	Leu
									25				30		

Lys	Pro	Ile	Ala	Gly	Phe	Ile	Thr	Gly	Asp	Gln	Ala	Arg	Asn	Phe	Phe
									40			45			

Phe	Gln	Ser	Gly	Leu	Pro	Gln	Pro	Val	Leu	Ala	Gln	Ile	Trp	Ala	Leu
									55			60			

Ala	Asp	Met	Asn	Asn	Asp	Gly	Arg	Met	Asp	Gln	Val	Glu	Phe	Ser	Ile
									70		75		80		

Ala	Met	Lys	Leu	Ile	Lys	Leu	Lys	Leu	Gln	Gly	Tyr	Gln	Leu	Pro	Ser
									85		90		95		

Thr	Leu	Pro	Pro	Val	Met	Lys	Gln	Gln	Pro	Val	Ala	Ile	Ser	Ser	Ala
									100		105		110		

Pro	Ala	Phe	Gly	Ile	Gly	Gly	Ile	Ala	Ser	Met	Pro	Pro	Leu	Thr	Ala
									115		120		125		

Val	Ala	Pro	Val	Pro	Met	Gly	Ser	Ile	Pro	Val	Val	Gly	Met	Ser	Pro
									130		135		140		

Pro	Leu	Val	Ser	Ser	Val	Pro	Pro	Ala	Ala	Val	Pro	Pro	Leu	Ala	Asn
									145		150		155		160

Gly	Ala	Pro	Pro	Val	Ile	Gln	Pro	Leu	Pro	Ala	Phe	Ala	His	Pro	Ala
									165		170		175		

Ala Thr Trp Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser
180 185 190

Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser
195 200 205

Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys
210 215 220

Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu
225 230 235 240

Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln
245 250 255

Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly
260 265 270

Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val
275 280 285

Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile
290 295 300

Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile
305 310 315 320

Ser Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu
325 330 335

Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys
340 345 350

Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg
355 360 365

Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln
370 375 380

Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln
385 390 395 400

Glu Ala Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln Arg
405 410 415

Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg
420 425 430

Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp
435 440 445

Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln
450 455 460

Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu
465 470 475 480

Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln
485 490 495

Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr
500 505 510

Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln
515 520 525

Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys
530 535 540

Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His
545 550 555 560

Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu
565 570 575

Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr
580 585 590

Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu
595 600 605

Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu
610 615 620

Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu
625 630 635 640

Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp
645 650 655

Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg
660 665 670

Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys
675 680 685

Lys Glu Ala Glu Glu Arg Ala Lys Pro Glu Met Gln Asp Lys Gln Ser
690 695 700

Arg Leu Phe His Pro His Gln Glu Pro Ala Lys Leu Ala Thr Gln Ala
705 710 715 720

Pro Trp Ser Thr Thr Glu Lys Gly Pro Leu Thr Ile Ser Ala Gln Glu
725 730 735

Ser Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg
740 745 750

Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp
755 760 765

Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly
770 775 780

Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro Glu Asn
785 790 795 800

Glu Val Pro Thr Pro Ala Lys Pro Val Thr Asp Leu Thr Ser Ala Pro
805 810 815

Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Pro Val Thr
820 825 830

Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe Ser Ser
835 840 845

Thr Trp Pro Ser Ser Asn Glu Lys Pro Glu Thr Asp Asn Trp Asp
850 855 860

Thr Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly Gln Leu
865 870 875 880

Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser Ser Pro
885 890 895

Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln Ala Gln

900

905

910

Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn Phe Asn
915 920 925

Lys Ser Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp Trp Phe
930 935 940

Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr Val Lys
945 950 955 960

Leu Ile Ser Gly Pro Val Arg Lys Ser Thr Ser Ile Asp Thr Gly Pro
965 970 975

Thr Glu Ser Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala Ala Lys
980 985 990

Pro Ala Ile Pro Gly Glu Glu Phe Ile Ala Met Tyr Thr Tyr Glu Ser
995 1000 1005

Ser Glu Gln Gly Asp Leu Thr Phe Gln Gln Gly Asp Val Ile Val
1010 1015 1020

Val Thr Lys Lys Asp Gly Asp Trp Trp Thr Gly Thr Val Gly Asp
1025 1030 1035

Lys Ser Gly Val Phe Pro Ser Asn Tyr Val Arg Leu Lys Asp Ser
1040 1045 1050

Glu Gly Ser Gly Thr Ala Gly Lys Thr Gly Ser Leu Gly Lys Lys
1055 1060 1065

Pro Glu Ile Ala Gln Val Ile Ala Ser Tyr Ala Ala Thr Gly Pro
1070 1075 1080

Glu Gln Leu Thr Leu Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys
1085 1090 1095

Lys Asn Pro Gly Gly Trp Trp Glu Gly Glu Leu Gln Ala Arg Gly
1100 1105 1110

Lys Lys Arg Gln Ile Gly Trp Phe Pro Ala Asn Tyr Val Lys Leu
1115 1120 1125

Leu Ser Pro Gly Thr Ser Lys Ile Thr Pro Thr Glu Leu Pro Lys
1130 1135 1140

Thr Ala Val Gln Pro Ala Val Cys Gln Val Ile Gly Met Tyr Asp
1145 1150 1155

Tyr Thr Ala Gln Asn Asp Asp Glu Leu Ala Phe Ser Lys Gly Gln
1160 1165 1170

Ile Ile Asn Val Leu Asn Lys Glu Asp Pro Asp Trp Trp Lys Gly
1175 1180 1185

Glu Val Ser Gly Gln Val Gly Leu Phe Pro Ser Asn Tyr Val Lys
1190 1195 1200

Leu Thr Thr Asp Met Asp Pro Ser Gln Gln Trp Cys Ser Asp Leu
1205 1210 1215

His Leu Leu Asp Met Leu Thr Pro Thr Glu Arg Lys Arg Gln Gly
1220 1225 1230

Tyr Ile His Glu Leu Ile Val Thr Glu Glu Asn Tyr Val Asn Asp
1235 1240 1245

Leu Gln Leu Val Thr Glu Ile Phe Gln Lys Pro Leu Thr Glu Ser
1250 1255 1260

Glu Leu Leu Thr Glu Lys Glu Val Ala Met Ile Phe Val Asn Trp
1265 1270 1275

Lys Glu Leu Ile Met Cys Asn Ile Lys Leu Leu Lys Ala Leu Arg
1280 1285 1290

Val Arg Lys Lys Met Ser Gly Glu Lys Met Pro Val Lys Met Ile
1295 1300 1305

Gly Asp Ile Leu Ser Ala Gln Leu Pro His Met Gln Pro Tyr Ile
1310 1315 1320

Arg Phe Cys Ser Cys Gln Leu Asn Gly Ala Ala Leu Ile Gln Gln
1325 1330 1335

Lys Thr Asp Glu Ala Pro Asp Phe Lys Glu Phe Val Lys Arg Leu
1340 1345 1350

Ala Met Asp Pro Arg Cys Lys Gly Met Pro Leu Ser Ser Phe Ile
1355 1360 1365

Leu Lys Pro Met Gln Arg Val Thr Arg Tyr Pro Leu Ile Ile Lys
1370 1375 1380

Asn Ile Leu Glu Asn Thr Pro Glu Asn His Pro Asp His Ser His
1385 1390 1395

Leu Lys His Ala Leu Glu Lys Ala Glu Glu Leu Cys Ser Gln Val
1400 1405 1410

Asn Glu Gly Val Arg Glu Lys Glu Asn Ser Asp Arg Leu Glu Trp
1415 1420 1425

Ile Gln Ala His Val Gln Cys Glu Gly Leu Ser Glu Gln Leu Val
1430 1435 1440

Phe Asn Ser Val Thr Asn Cys Leu Gly Pro Arg Lys Phe Leu His
1445 1450 1455

Ser Gly Lys Leu Tyr Lys Ala Lys Ser Asn Lys Glu Leu Tyr Gly
1460 1465 1470

Phe Leu Phe Asn Asp Phe Leu Leu Leu Thr Gln Ile Thr Lys Pro
1475 1480 1485

Leu Gly Ser Ser Gly Thr Asp Lys Val Phe Ser Pro Lys Ser Asn
1490 1495 1500

Leu Gln Tyr Lys Met Tyr Lys Thr Pro Ile Phe Leu Asn Glu Val
1505 1510 1515

Leu Val Lys Leu Pro Thr Asp Pro Ser Gly Asp Glu Pro Ile Phe
1520 1525 1530

His Ile Ser His Ile Asp Arg Val Tyr Thr Leu Arg Ala Glu Ser
1535 1540 1545

Ile Asn Glu Arg Thr Ala Trp Val Gln Lys Ile Lys Ala Ala Ser
1550 1555 1560

Glu Leu Tyr Ile Glu Thr Glu Lys Lys Lys Arg Glu Lys Ala Tyr
1565 1570 1575

Leu Val Arg Ser Gln Arg Ala Thr Gly Ile Gly Arg Leu Met Val
1580 1585 1590

Asn Val Val Glu Gly Ile Glu Leu Lys Pro Cys Arg Ser His Gly
1595 1600 1605

Lys Ser Asn Pro Tyr Cys Glu Val Thr Met Gly Ser Gln Cys His
1610 1615 1620

Ile Thr Lys Thr Ile Gln Asp Thr Leu Asn Pro Lys Trp Asn Ser
1625 1630 1635

Asn Cys Gln Phe Phe Ile Arg Asp Leu Glu Gln Glu Val Leu Cys
1640 1645 1650

Ile Thr Val Phe Glu Arg Asp Gln Phe Ser Pro Asp Asp Phe Leu
1655 1660 1665

Gly Arg Thr Glu Ile Arg Val Ala Asp Ile Lys Lys Asp Gln Gly
1670 1675 1680

Ser Lys Gly Pro Val Thr Lys Cys Leu Leu Leu His Glu Val Pro
1685 1690 1695

Thr Gly Glu Ile Val Val Arg Leu Asp Leu Gln Leu Phe Asp Glu
1700 1705 1710

Pro

<210> 25
<211> 6014
<212> DNA
<213> Mus musculus

<400> 25		
cccttccttt ctttttttg tgttcgctt cggccgtgcc ggctgagagc ccagcagccg	60	
tgacaggctg cgcaacaggt tcgctcgcc cggcctgacg actgacccgg cggcggcggc	120	
cgcggcacgg cagggtcttc cggagcttg gccgcgcaca cgccgggtg tcgaggagcg	180	
cgcgggtcg cgccgggacg tgcgcgaggc gccagatggc tgagagctgc aagaagaagt	240	
caggatcatg atggctcagt ttcccacagc gatgaatgga gggccaaata tgtggctat	300	
tacatctgaa gaacgtacta agcatgataa acagttgtat aacctaacc cttcaggagg	360	
ttacataaca ggtgatcaag cccgtacttt tttcctacag tcaggtctgc cggccccgt	420	
tttagctgaa atatgggcct tatcagatct gaacaaggat gggaaagatgg accagcaaga	480	
gttctctata gctatgaaac tcatcaagtt aaagttgcag gccaacagc tgcctgttagt	540	
cctccctcct atcatgaaac aacccctat gttctctcca ctaatctctg ctcgtttgg	600	

gatgggaagc atgcccattc	660
tcagccattt cctccagttt	
cacctatagc aacaccctt	720
gcttctgcta cgtcagggac	
cagtattctt cccctaattt	
tgccctgtcc cctagtgctt	780
tctgttagt catcctcatt	
accaaatggactgcccagtc	
tcattcagcc tttatccatt	840
cottattctt cttcaacatt	
gcctcatgca tcatcttaca	
gcctgtatgt gggaggattt	900
ggtggtgcta gtatccagaa	
ggcccagtc tctgattgatt	
taggatctatgctcaact	960
tcctcaactg cttccctctc	
agggaaactca cctaagacag	
ggacctcaga gtgggcagtt	1020
cctcagcctt caagattaaa	
gtatcgaa aaatttataa	
gtctagacaa aggcatgagc	1080
ggataccctt caggtttca	
agctagaaat gcccttcttc	
agtcaaactct cttctcaaact	1140
cagctagcta ctatttggac	
tctggctgac atcgatggtg	
acggacagtt gaaagctgaa	1200
gaatttattt tggcgatgca	
cctcactgac atggccaaag	
ctggacagcc actaccactg	1260
acgttgcctc ccgagcttgt	
ccctccatct ttcagagggg	
gaaagcaagt tgattctgtt	1320
aatggaaactc tgccttcata	
tcagaaaaca caagaagaag	
agcctcagaa gaaactgcca	1380
gttactttt aggacaaacg	
gaaagccaaat tatgaacgag	
gaaacatggcgatggagaag	1440
cgacgccaag ttttgatgga	
gcagcagcag agggaggctg	
aacgcaaaagc ccagaaagag	1500
aaggaagagt gggagcggaa	
acagagagaa ctgcaagagc	
aagaatggaa gaagcagctg	1560
gagttggaga aacgcttggaa	
gaaacagaga gagctggaga	
gacagcggga ggaagagagg	1620
agaaaaggaga tagaaagacg	
agagggcagca aaacaggago	
ttgagagaca acgcccgttta	1680
gaatggaaa gactccgtcg	
gcaggagctg ctcagtcaga	
agaccaggga acaagaagac	1740
attgtcaggc tgagctccag	
aaagaaaagt ctcacacctgg	
aactggaaagc agtgaatggaa	1800
aaacatcagc agatctcagg	
cagactacaa gatgtccaaa	
tcagaaagca aacacaaaag	1860
actgagctg aagttttggaa	
taaacagtgt gacctggaaa	
ttatggaaat caaacaactt	1920
caacaagagc ttaaggaata	
tcaaaataag cttatctatc	
tggtccctga gaagcagcta	1980
ttaaaacgaaa gaattaaaaa	
catgcagctc agtaacacac	
ctgattcagg gatcagttta	2040
cttcataaaaa agtcatcaga	
aaaggaagaa ttatgccaaa	
gacttaaaga acaatttagat	2100
gctcttgaaa aagaaactgc	
atctaagctc tcagaaatgg	
attcatttaa caatcagctg	2160
aaggaactca gagaaagcta	
taatacacag cagttagccc	
ttgaacaact tcataaaaatc	2220
aaacgtgaca aattgaagga	
aatcgaaaga aaaagattag	
agcaaattca aaaaaagaaa	2280
ctagaagatg aggctgcaag	
gaaagcaaag caaggaaaag	
aaaacttgc gagagaaaagt	2340
attagaaagg aagaagagga	
aaagcaaaaa cgactccagg	
aagaaaagtc acaggacaaa	2400
actcaagaag aggaacgaaa	
agctgaggca aaacaaagtg	
agacagccag	

tgctttggtg aattacagag cactgtaccc ttttgaagca agaaaccatg atgagatgag	2460
tttttagttct ggggatataa ttcaggttga tgaaaaaact gtaggagagc ctggttggct	2520
ttatggtagt ttccagggaa agtttggctg gttccctgc aactatgtag aaaaagtgt	2580
gtcaagtgaa aaagctctgt ctccctaagaa ggccttactt ctcctacag tgtctcttc	2640
tgctacctca acttcttccc agccaccagc atcagtgact gattatcaca atgtatcctt	2700
ctcaaacctt actgttaata caacatggca gcagaagtca gctttaccc gcactgtgtc	2760
ccctggatct gtgtccccca ttcacggaca ggggcaggct gtagaaaacc tgaaagccca	2820
ggccctttgt tcctggacgg caaagaagga gaaccacctg aacttctcaa agcacgacgt	2880
catcactgtc ctggagcagc aggaaaactg gtggtttggg gaggtgcacg gaggaagagg	2940
atggttcccc aagtcttatg tcaagctcat tcctggaaat gaagtacagc gaggagagcc	3000
agaagctttg tatgcagctg tgactaagaa acctacctcc acagcctatc cagttacctc	3060
cacagcctat ccagttggag aagactacat tgcactttat tcatactcaa gtgtagagcc	3120
cggggatttg actttcactg aaggtgaaga aattcttagtg acccagaaag atggagagtg	3180
gtggacagga agtattggag agagaactgg aatcttcccg tccaactacg tcagaccaaa	3240
ggatcaagag aattttggga atgctagcaa atctggagca tcaaacaaaa aacccgagat	3300
cgctcaagta acttcagcat atgctgcttc agggactgag cagctcagcc ttgcgcagg	3360
acagttataa ttaatcttaa agaaaaacac aagcgggtgg tggcaaggag agctacaggc	3420
cagagggaaag aaacgcacaga agggatggtt tcctgccagc catgtaaagc tgcttagtcc	3480
aagcagtgaa agaaccatgc ctactttca cgctgtatgt caagtgattg ctatgtatga	3540
ctacatggcg aataacgaag atgagctaa tttctccaaa ggacagctga ttaatgttat	3600
gaacaaagat gaccctgact ggtggcaagg agaaaccaat ggtctgactg gtctcttcc	3660
ttcaaactat gttaagatga caacagactc agatccaatg caacagtggt gtgctgaccc	3720
ccaagccctg gacacaatgc agcctacgga gaggaagcga cagggctaca ttcacgagct	3780
cattcagaca gaggagcggt acatggacga cgacctgcag ctggtcatcg aggtcttcca	3840
gaaacggatg gctgaggaag gttccctcac tgaagcagac atggctctga tctttgtgaa	3900
ctggaaagag ctcatcatgt ccaacacgaa gctgctgagg gccttgcggg tgaggaagaa	3960
gactgggggt gagaagatgc cagttcagat gattggagac atcctggcgg cagagctgtc	4020
ccacatgcag gcttacatcc gttctgcag ctgtcagctt aatggggcaa ccctgttaca	4080
gcagaagaca gacgaggaca cggacttcaa ggaatttcta aagaagttgg catcagaccc	4140
acgatgcaaa gggatgcccc tctccagctt cctgctgaag cccatgcaga ggatcactcg	4200
ctaccgcgtc ctcatccgaa gtatcctgga gaacactcca cagagtcatg ttgaccactc	4260

ctccctgaag ctggccctag aacgtgctga ggagctgtgc ttcaggtga acgagggagt	4320
ccgggagaag gaaaattcag accggctgga gtggatccag gcacacgtgc agtgcgaagg	4380
cttggcagag caacttattt tcaactccct caccactgc ctggggcccc ggaagcttct	4440
gcacagcggg aagctgtaca agaccaagag caataaggag ctgcacgcct tcctttcaa	4500
cgacttcctg ctgctcacct acctggtcag gcagttgcc gccgcctctg gccacgagaa	4560
gctcttcaac tccaagtcca gtgctcagtt ccggatgtac aaaacgccc tttcctgaa	4620
tgaagtgtt gtaaaacttc ccacagaccc ttccggcgat gagcccgct tccacatttc	4680
ccacattgat cgtgtgtaca cactccgaac agacaacatc aacgagagga cggcctgggt	4740
ccagaagatc aagggtgcct cagagcagta catcgacact gagaagaaga aacgggaaaa	4800
ggcttaccaa gcccgttctc aaaagacttc aggtattggg cgtctgatgg tgcatgtcat	4860
tgaagctaca gaattaaaag cctgcaaacc aaacgggaaa agtaatccat actgtgaagt	4920
cagcatgggc tcccaaagct ataccaccag gaccctgcag gacacactaa accccaagtg	4980
gaacttcaac tgccagttct tcatcaagga tcttaccag gacgttctgt gtctcactat	5040
gttgacaga gaccagttt ctccagatga cttcttgggt cgtactgaag ttccagtggc	5100
aaaaatccga acagaacagg aaagcaaagg ccccaccacc cgccgactac tactgcacga	5160
agtccccact ggagaagtct gggccgctt tgacctgcaa cttttgaac aaaaaactct	5220
ccttgaggg cctggggaaag ccagaaccag gggagctgcc cacaaggctg ggtctaaaga	5280
cagatttgc tctcccagga cagaggagca tcacatggct tcatccatca aacagccaca	5340
ctcgctggc ctgtatTTtta ttgcacacta aattgcttagc aatctatgca aacatgatct	5400
tttaaacaaa cgcacagca cagtgcctg tactagtgtt aacctgttca gctgtgttag	5460
atgccagggt ttccatTTtc agggctataa aagtattatg tggaaatgag gcatcagacc	5520
accggacgtt accacttggc aaatctgtcc actgtggagt tggtgatgtt ggaaccattc	5580
cacactatgt gacctctgct ggtcacaca ctcaggaggt gaagggctga gatgaaatgc	5640
tgcagccttgc gggcttgc agcctgatac taaaatagca tccacttgc cactgaataa	5700
atagaaactt gatgtttta ttctgacttag atattatcat tctctgctaa gacaatata	5760
tttggaaatata tataaggag gaaagctga tgtactttaa atataactgtg	5820
aactctaata atgtggggat attttcaac tttatTTtc ttaagtataa attattatg	5880
taaattcttt gtttgcata tttcatagaa catgcattt taagctttat cattgccaac	5940
aatgtacaga aagagaataa aagtataagt ttatgaatgt aaaaaaaaaa aaaaaaaaaa	6000
aaaaaaaaaaa aaaa	6014

<210> 26
 <211> 4977
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(4977)
 <223> Mouse Ese2L

<400> 26

atg	gct	cag	ttt	ccc	aca	gca	atg	aat	gga	ggg	cca	aat	atg	tgg	gct	48
Met	Ala	Gln	Phe	Pro	Thr	Ala	Met	Asn	Gly	Gly	Pro	Asn	Met	Trp	Ala	
1			5				10					15				

att aca tct gaa gaa cgt act aag cat gat aaa cag ttt gat aac ctc

Ile	Thr	Ser	Glu	Glu	Arg	Thr	Lys	His	Asp	Lys	Gln	Phe	Asp	Asn	Leu	96
20				25					30							

aaa cct tca gga ggt tac ata aca ggt gat caa gcc cgt act ttt ttc

Lys	Pro	Ser	Gly	Gly	Tyr	Ile	Thr	Gly	Asp	Gln	Ala	Arg	Thr	Phe	Phe	144
35				40					45							

cta cag tca ggt ctg ccg gcc ccg gtt tta gct gaa ata tgg gcc tta

Leu	Gln	Ser	Gly	Leu	Pro	Ala	Pro	Val	Leu	Ala	Glu	Ile	Trp	Ala	Leu	192
50				55					60							

tca gat ctg aac aag gat ggg aag atg gac cag caa gag ttc tct ata

Ser	Asp	Leu	Asn	Lys	Asp	Gly	Lys	Met	Asp	Gln	Gln	Glu	Phe	Ser	Ile	240
65				70				75				80				

gct atg aaa ctc atc aag tta aag ttg cag ggc caa cag ctg cct gta

Ala	Met	Lys	Leu	Ile	Lys	Leu	Lys	Leu	Gln	Gly	Gln	Gln	Leu	Pro	Val	288
85					90							95				

gtc ctc cct atc atg aaa caa ccc cct atg ttc tct cca cta atc

Val	Leu	Pro	Pro	Ile	Met	Lys	Gln	Pro	Pro	Met	Phe	Ser	Pro	Leu	Ile	336
100					105							110				

tct gct cgt ttt ggg atg gga agc atg ccc aat ctg tcc att cat cag

Ser	Ala	Arg	Phe	Gly	Met	Gly	Ser	Met	Pro	Asn	Leu	Ser	Ile	His	Gln	384
115					120							125				

cca ttg cct cca gtt gca cct ata gca aca ccc ttg tct tct gct acg

Pro	Leu	Pro	Pro	Val	Ala	Pro	Ile	Ala	Thr	Pro	Leu	Ser	Ser	Ala	Thr	432
130					135				140							

tca ggg acc agt att cct ccc cta atg atg cct gct ccc cta gtg cct

Ser	Gly	Thr	Ser	Ile	Pro	Pro	Leu	Met	Met	Pro	Ala	Pro	Leu	Val	Pro	480
145					150			155		160						

tct gtt agt aca tcc tca tta cca aat gga act gcc agt ctc att cag

Ser	Val	Ser	Thr	Ser	Ser	Leu	Pro	Asn	Gly	Thr	Ala	Ser	Leu	Ile	Gln	528
165					170				175							

cct tta tcc att cct tat tct tct tca aca ttg cct cat gca tca tct

Pro	Leu	Ser	Ile	Pro	Tyr	Ser	Ser	Ser	Thr	Leu	Pro	His	Ala	Ser	Ser	576
180					185				190							

tac agc ctg atg atg gga gga ttt ggt ggt gct agt atc cag aag gcc Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala 195 200 205	624
cag tct ctg att gat tta gga tct agt agc tca act tcc tca act gct Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Thr Ser Ser Thr Ala 210 215 220	672
tcc ctc tca ggg aac tca cct aag aca ggg acc tca gag tgg gca gtt Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val 225 230 235 240	720
cct cag cct tca aga tta aag tat cgg caa aaa ttt aat agt cta gac Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp 245 250 255	768
aaa ggc atg agc gga tac ctc tca ggt ttt caa gct aga aat gcc ctt Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu 260 265 270	816
ctt cag tca aat ctc tct caa act cag cta gct act att tgg act ctg Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu 275 280 285	864
gct gac atc gat ggt gac gga cag ttg aaa gct gaa gaa ttt att ctg Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu 290 295 300	912
gcg atg cac ctc act gac atg gcc aaa gct gga cag cca cta cca ctg Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu 305 310 315 320	960
acg ttg cct ccc gag ctt gtc cct cca tct ttc aga ggg gga aag caa Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln 325 330 335	1008
gtt gat tct gtt aat gga act ctg cct tca tat cag aaa aca caa gaa Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu 340 345 350	1056
gaa gag cct cag aag aaa ctg cca gtt act ttt gag gac aaa cgg aaa Glu Glu Pro Gln Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys 355 360 365	1104
gcc aac tat gaa cga gga aac atg gag ctg gag aag cga cgc caa gtg Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val 370 375 380	1152
ttg atg gag cag cag agg gag gct gaa cgc aaa gcc cag aaa gag Leu Met Glu Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu 385 390 395 400	1200
aag gaa gag tgg gag cgg aaa cag aga gaa ctg caa gag caa gaa tgg Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp 405 410 415	1248
aag aag cag ctg gag ttg gag aaa cgc ttg gag aaa cag aga gag ctg Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu 420 425 430	1296
gag aga cag cgg gag gaa gag agg aga aag gag ata gaa aga cga gag	1344

Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu			
435	440	445	
gca gca aaa cag gag ctt gag aga caa cgc cgt tta gaa tgg gaa aga		1392	
Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg			
450	455	460	
ctc cgt cgg cag gag ctg ctc agt cag aag acc agg gaa caa gaa gac		1440	
Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp			
465	470	475	480
att gtc agg ctg agc tcc aga aag aaa agt ctc cac ctg gaa ctg gaa		1488	
Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu			
485	490	495	
gca gtg aat gga aaa cat cag cag atc tca ggc aga cta caa gat gtc		1536	
Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val			
500	505	510	
caa atc aga aag caa aca caa aag act gag cta gaa gtt ttg gat aaa		1584	
Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys			
515	520	525	
cag tgt gac ctg gaa att atg gaa atc aaa caa ctt caa caa gag ctt		1632	
Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu			
530	535	540	
aag gaa tat caa aat aag ctt atc tat ctg gtc cct gag aag cag cta		1680	
Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu			
545	550	555	560
tta aac gaa aga att aaa aac atg cag ctc agt aac aca cct gat tca		1728	
Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser			
565	570	575	
ggg atc agt tta ctt cat aaa aag tca tca gaa aag gaa gaa tta tgc		1776	
Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys			
580	585	590	
caa aga ctt aaa gaa caa tta gat gct ctt gaa aaa gaa act gca tct		1824	
Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser			
595	600	605	
aag ctc tca gaa atg gat tca ttt aac aat cag ctg aag gaa ctc aga		1872	
Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg			
610	615	620	
gaa agc tat aat aca cag cag tta gcc ctt gaa caa ctt cat aaa atc		1920	
Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile			
625	630	635	640
aaa cgt gac aaa ttg aag gaa atc gaa aga aaa aga tta gag caa att		1968	
Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile			
645	650	655	
caa aaa aag aaa cta gaa gat gag gct gca agg aaa gca aag caa gga		2016	
Gln Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly			
660	665	670	
aaa gaa aac ttg tgg aga gaa agt att aga aag gaa gaa gag gaa aag		2064	
Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Lys			

675	680	685	
caa aaa cga ctc cag gaa gaa aag tca cag gac aaa act caa gaa gag Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu 690	695	700	2112
gaa cga aaa gct gag gca aaa caa agt gag aca gcc agt gct ttg gtg Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val 705	710	715	2160
aat tac aga gca ctg tac cct ttt gaa gca aga aac cat gat gag atg Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met 725	730	735	2208
agt ttt agt tct ggg gat ata att cag gtt gat gaa aaa act gta gga Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly 740	745	750	2256
gag cct ggt tgg ctt tat ggt agt ttt cag gga aag ttt ggc tgg ttc Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe 755	760	765	2304
ccc tgc aac tat gta gaa aaa gtg ctg tca agt gaa aaa gct ctg tct Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser 770	775	780	2352
cct aag aag gcc tta ctt cct cct aca gtg tct ctc tct gct acc tca Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser 785	790	795	2400
act tct tcc cag cca cca gca tca gtg act gat tat cac aat gta tcc Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser 805	810	815	2448
ttc tca aac ctt act gtt aat aca aca tgg cag cag aag tca gct ttt Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe 820	825	830	2496
acc cgc act gtg tcc cct gga tct gtg tcc ccc att cac gga cag ggg Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly 835	840	845	2544
cag gct gta gaa aac ctg aaa gcc cag gcc ctt tgg acg gca Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala 850	855	860	2592
aag aag gag aac cac ctg aac ttc tca aag cac gac gtc atc act gtc Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val 865	870	875	2640
ctg gag cag cag gaa aac tgg tgg ttt ggg gag gtg cac gga gga aga Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg 885	890	895	2688
gga tgg ttc ccc aag tct tat gtc aag ctc att cct ggg aat gaa gta Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val 900	905	910	2736
cag cga gga gag cca gaa gct ttg tat gca gct gtg act aag aaa cct Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro 915	920	925	2784

acc tcc aca gcc tat cca gtt acc tcc aca gcc tat cca gtt gga gaa	2832
Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu	
930 935 940	
gac tac att gca ctt tat tca tac tca agt gta gag ccc ggg gat ttg	2880
Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Val Glu Pro Gly Asp Leu	
945 950 955 960	
act ttc act gaa ggt gaa gaa att cta gtg acc cag aaa gat gga gag	2928
Thr Phe Thr Glu Gly Glu Ile Leu Val Thr Gln Lys Asp Gly Glu	
965 970 975	
tgg tgg aca gga agt att gga gag aga act gga atc ttc ccg tcc aac	2976
Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn	
980 985 990	
tac gtc aga cca aag gat caa gag aat ttt ggg aat gct agc aaa tct	3024
Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser	
995 1000 1005	
gga gca tca aac aaa aaa ccc gag atc gct caa gta act tca gca	3069
Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala	
1010 1015 1020	
tat gct gct tca ggg act gag cag ctc agc ctt gcg cca gga cag	3114
Tyr Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln	
1025 1030 1035	
tta ata tta atc tta aag aaa aac aca agc ggg tgg tgg caa gga	3159
Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly	
1040 1045 1050	
gag cta cag gcc aga ggg aag aaa cga cag aag gga tgg ttt cct	3204
Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro	
1055 1060 1065	
gcc agc cat gta aag ctg cta ggt cca agc agt gaa aga acc atg	3249
Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met	
1070 1075 1080	
cct act ttt cac gct gta tgt caa gtg att gct atg tat gac tac	3294
Pro Thr Phe His Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr	
1085 1090 1095	
atg gcg aat aac gaa gat gag ctc aat ttc tcc aaa gga cag ctg	3339
Met Ala Asn Asn Glu Asp Glu Leu Asn Phe Ser Lys Gly Gln Leu	
1100 1105 1110	
att aat gtt atg aac aaa gat gac cct gac tgg tgg caa gga gaa	3384
Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu	
1115 1120 1125	
acc aat ggt ctg act ggt ctc ttt cct tca aac tat gtt aag atg	3429
Thr Asn Gly Leu Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met	
1130 1135 1140	
aca aca gac tca gat cca agt caa cag tgg tgt gct gac ctc caa	3474
Thr Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln	
1145 1150 1155	

gcc	ctg	gac	aca	atg	cag	cct	acg	gag	agg	aag	cga	cag	ggc	tac	3519
Ala	Leu	Asp	Thr	Met	Gln	Pro	Thr	Glu	Arg	Lys	Arg	Gln	Gly	Tyr	
1160					1165						1170				
att	cac	gag	ctc	att	cag	aca	gag	gag	cgg	tac	atg	gac	gac	gac	3564
Ile	His	Glu	Leu	Ile	Gln	Thr	Glu	Glu	Arg	Tyr	Met	Asp	Asp	Asp	
1175					1180						1185				
ctg	cag	ctg	gtc	atc	gag	gtc	ttc	cag	aaa	cgg	atg	gct	gag	gaa	3609
Leu	Gln	Leu	Val	Ile	Glu	Val	Phe	Gln	Lys	Arg	Met	Ala	Glu	Glu	
1190					1195						1200				
ggc	tcc	ctc	act	gaa	gca	gac	atg	gct	ctg	atc	ttt	gtg	aac	tgg	3654
Gly	Phe	Leu	Thr	Glu	Ala	Asp	Met	Ala	Leu	Ile	Phe	Val	Asn	Trp	
1205					1210						1215				
aaa	gag	ctc	atc	atg	tcc	aac	acg	aag	ctg	ctg	agg	gcc	ttg	cgg	3699
Lys	Glu	Leu	Ile	Met	Ser	Asn	Thr	Lys	Leu	Leu	Arg	Ala	Leu	Arg	
1220					1225						1230				
gtg	agg	aag	aag	act	ggg	ggt	gag	aag	atg	cca	gtt	cag	atg	att	3744
Val	Arg	Lys	Lys	Thr	Gly	Gly	Glu	Lys	Met	Pro	Val	Gln	Met	Ile	
1235					1240						1245				
gga	gac	atc	ctg	gcg	gca	gag	ctg	tcc	cac	atg	cag	gcc	tac	atc	3789
Gly	Asp	Ile	Leu	Ala	Ala	Glu	Leu	Ser	His	Met	Gln	Ala	Tyr	Ile	
1250					1255						1260				
cgc	ttc	tgc	agc	tgt	cag	ctt	aat	ggg	gca	acc	ctg	tta	cag	cag	3834
Arg	Phe	Cys	Ser	Cys	Gln	Leu	Asn	Gly	Ala	Thr	Leu	Leu	Gln	Gln	
1265					1270						1275				
aag	aca	gac	gag	gac	acg	gac	ttc	aag	gaa	ttt	cta	aag	aag	ttg	3879
Lys	Thr	Asp	Glu	Asp	Thr	Asp	Phe	Lys	Glu	Phe	Leu	Lys	Lys	Leu	
1280					1285						1290				
gca	tca	gac	cca	cga	tgc	aaa	ggg	atg	ccc	ctc	tcc	agc	ttc	ctg	3924
Ala	Ser	Asp	Pro	Arg	Cys	Lys	Gly	Met	Pro	Leu	Ser	Ser	Phe	Leu	
1295					1300						1305				
ctg	aag	ccc	atg	cag	agg	atc	act	cgc	tac	ccg	ctg	ctc	atc	cga	3969
Leu	Lys	Pro	Met	Gln	Arg	Ile	Thr	Arg	Tyr	Pro	Leu	Leu	Ile	Arg	
1310					1315						1320				
agt	atc	ctg	gag	aac	act	cca	cag	agt	cat	gtt	gac	cac	tcc	tcc	4014
Ser	Ile	Leu	Glu	Asn	Thr	Pro	Gln	Ser	His	Val	Asp	His	Ser	Ser	
1325					1330						1335				
ctg	aag	ctg	gcc	cta	gaa	cgt	gct	gag	gag	ctg	tgc	tct	cag	gtg	4059
Leu	Lys	Leu	Ala	Leu	Glu	Arg	Ala	Glu	Glu	Leu	Cys	Ser	Gln	Val	
1340					1345						1350				
aac	gag	gga	gtc	cgg	gag	aag	gaa	aat	tca	gac	cgg	ctg	gag	tgg	4104
Asn	Glu	Gly	Val	Arg	Glu	Lys	Glu	Asn	Ser	Asp	Arg	Leu	Glu	Trp	
1355					1360						1365				
atc	cag	gca	cac	gtg	cag	tgc	gaa	ggc	ttt	gca	gag	caa	ctt	att	4149
Ile	Gln	Ala	His	Val	Gln	Cys	Glu	Gly	Leu	Ala	Glu	Gln	Leu	Ile	
1370					1375						1380				
ttc	aac	tcc	ctc	acc	aac	tgc	ctg	ggc	ccc	cgg	aag	ctt	ctg	cac	4194

Phe	Asn	Ser	Leu	Thr	Asn	Cys	Leu	Gly	Pro	Arg	Lys	Leu	Leu	His	
1385						1390					1395				
agc	ggg	aag	ctg	tac	aag	acc	aag	agc	aat	aag	gag	ctg	cac	gcc	4239
Ser	Gly	Lys	Leu	Tyr	Lys	Thr	Lys	Ser	Asn	Lys	Glu	Leu	His	Ala	
1400						1405					1410				
tcc	ctc	ttc	aac	gac	ttc	ctg	ctg	ctc	acc	tac	ctg	gtc	agg	cag	4284
Phe	Leu	Phe	Asn	Asp	Phe	Leu	Leu	Leu	Thr	Tyr	Leu	Val	Arg	Gln	
1415						1420					1425				
ttt	gcc	gcc	gcc	tct	ggc	cac	gag	aag	ctc	ttc	aac	tcc	aag	tcc	4329
Phe	Ala	Ala	Ala	Ser	Gly	His	Glu	Lys	Leu	Phe	Asn	Ser	Lys	Ser	
1430						1435					1440				
agt	gct	cag	ttc	cgg	atg	tac	aaa	acg	ccc	att	ttc	ctg	aat	gaa	4374
Ser	Ala	Gln	Phe	Arg	Met	Tyr	Lys	Thr	Pro	Ile	Phe	Leu	Asn	Glu	
1445						1450					1455				
gtg	ttg	gtg	aaa	ctt	ccc	aca	gac	cct	tcc	ggc	gat	gag	ccc	gtc	4419
Val	Leu	Val	Lys	Leu	Pro	Thr	Asp	Pro	Ser	Gly	Asp	Glu	Pro	Val	
1460						1465					1470				
ttc	cac	att	tcc	cac	att	gat	cgt	gtg	tac	aca	ctc	cga	aca	gac	4464
Phe	His	Ile	Ser	His	Ile	Asp	Arg	Val	Tyr	Thr	Leu	Arg	Thr	Asp	
1475						1480					1485				
aac	atc	aac	gag	agg	acg	gcc	tgg	gtc	cag	aag	atc	aag	ggt	gcc	4509
Asn	Ile	Asn	Glu	Arg	Thr	Ala	Trp	Val	Gln	Lys	Ile	Lys	Gly	Ala	
1490						1495					1500				
tca	gag	cag	tac	atc	gac	act	gag	aag	aag	aaa	cgg	gaa	aag	gct	4554
Ser	Glu	Gln	Tyr	Ile	Asp	Thr	Glu	Lys	Lys	Lys	Arg	Glu	Lys	Ala	
1505						1510					1515				
tac	caa	gcc	cgt	tct	caa	aag	act	tca	ggt	att	ggg	cgt	ctg	atg	4599
Tyr	Gln	Ala	Arg	Ser	Gln	Lys	Thr	Ser	Gly	Ile	Gly	Arg	Leu	Met	
1520						1525					1530				
gtg	cat	gtc	att	gaa	gct	aca	gaa	tta	aaa	gcc	tgc	aaa	cca	aac	4644
Val	His	Val	Ile	Glu	Ala	Thr	Glu	Leu	Lys	Ala	Cys	Lys	Pro	Asn	
1535						1540					1545				
ggg	aaa	agt	aat	cca	tac	tgt	gaa	gtc	agc	atg	ggc	tcc	caa	agc	4689
Gly	Lys	Ser	Asn	Pro	Tyr	Cys	Glu	Val	Ser	Met	Gly	Ser	Gln	Ser	
1550						1555					1560				
tat	acc	acc	agg	acc	ctg	cag	gac	aca	cta	aac	ccc	aag	tgg	aac	4734
Tyr	Thr	Thr	Arg	Thr	Leu	Gln	Asp	Thr	Leu	Asn	Pro	Lys	Trp	Asn	
1565						1570					1575				
ttc	aac	tgc	cag	ttc	ttc	atc	aag	gat	ctt	tac	cag	gac	gtt	ctg	4779
Phe	Asn	Cys	Gln	Phe	Phe	Ile	Lys	Asp	Leu	Tyr	Gln	Asp	Val	Leu	
1580						1585					1590				
tgt	ctc	act	atg	ttt	gac	aga	gac	cag	ttt	tct	cca	gat	gac	ttc	4824
Cys	Leu	Thr	Met	Phe	Asp	Arg	Asp	Gln	Phe	Ser	Pro	Asp	Asp	Phe	
1595						1600					1605				
ttg	ggt	cgt	act	gaa	gtt	cca	gtg	gca	aaa	atc	cga	aca	gaa	cag	4869
Leu	Gly	Arg	Thr	Glu	Val	Pro	Val	Ala	Lys	Ile	Arg	Thr	Glu	Gln	

1610	1615	1620	
gaa agc aaa ggc ccc acc acc	cgc cga cta cta ctg	cac gaa gtc	4914
Glu Ser Lys Gly Pro Thr Thr	Arg Arg Leu Leu Leu	His Glu Val	
1625	1630	1635	
ccc act gga gaa gtc tgg gtc	cgc ttt gac ctg caa	ctt ttt gaa	4959
Pro Thr Gly Glu Val Trp Val	Arg Phe Asp Leu Gln	Leu Phe Glu	
1640	1645	1650	
caa aaa act ctc ctt tga			4977
Gln Lys Thr Leu Leu			
1655			
<210> 27			
<211> 1658			
<212> PRT			
<213> Mus musculus			
<400> 27			
Met Ala Gln Phe Pro Thr Ala Met Asn Gly Gly Pro Asn Met Trp Ala			
1	5	10	15
Ile Thr Ser Glu Glu Arg Thr Lys His Asp Lys Gln Phe Asp Asn Leu			
20	25	30	
Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe			
35	40	45	
Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu			
50	55	60	
Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile			
65	70	75	80
Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val			
85	90	95	
Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile			
100	105	110	
Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln			
115	120	125	
Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr			
130	135	140	
Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro			
145	150	155	160

Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln
165 170 175

Pro Leu Ser Ile Pro Tyr Ser Ser Thr Leu Pro His Ala Ser Ser
180 185 190

Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala
195 200 205

Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala
210 215 220

Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val
225 230 235 240

Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp
245 250 255

Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu
260 265 270

Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu
275 280 285

Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu
290 295 300

Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu
305 310 315 320

Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln
325 330 335

Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu
340 345 350

Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys
355 360 365

Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val
370 375 380

Leu Met Glu Gln Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu
385 390 395 400

Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp
405 410 415

Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu
420 425 430

Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu
435 440 445

Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg
450 455 460

Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp
465 470 475 480

Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu
485 490 495

Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val
500 505 510

Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys
515 520 525

Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu
530 535 540

Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu
545 550 555 560

Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser
565 570 575

Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys
580 585 590

Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser
595 600 605

Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg
610 615 620

Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile
625 630 635 640

Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile

645

650

655

Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly
 660 665 670

Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Lys
 675 680 685

Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu
 690 695 700

Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val
 705 710 715 720

Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met
 725 730 735

Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly
 740 745 750

Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe
 755 760 765

Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser
 770 775 780

Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser
 785 790 795 800

Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser
 805 810 815

Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe
 820 825 830

Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly
 835 840 845

Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala
 850 855 860

Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val
 865 870 875 880

Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg
 885 890 895

Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val
900 905 910

Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro
915 920 925

Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu
930 935 940

Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu
945 950 955 960

Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu
965 970 975

Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn
980 985 990

Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser
995 1000 1005

Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala
1010 1015 1020

Tyr Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln
1025 1030 1035

Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly
1040 1045 1050

Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro
1055 1060 1065

Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met
1070 1075 1080

Pro Thr Phe His Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr
1085 1090 1095

Met Ala Asn Asn Glu Asp Glu Leu Asn Phe Ser Lys Gly Gln Leu
1100 1105 1110

Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu
1115 1120 1125

Thr Asn Gly Leu Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met
1130 1135 1140

Thr Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln
1145 1150 1155

Ala Leu Asp Thr Met Gln Pro Thr Glu Arg Lys Arg Gln Gly Tyr
1160 1165 1170

Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr Met Asp Asp Asp
1175 1180 1185

Leu Gln Leu Val Ile Glu Val Phe Gln Lys Arg Met Ala Glu Glu
1190 1195 1200

Gly Phe Leu Thr Glu Ala Asp Met Ala Leu Ile Phe Val Asn Trp
1205 1210 1215

Lys Glu Leu Ile Met Ser Asn Thr Lys Leu Leu Arg Ala Leu Arg
1220 1225 1230

Val Arg Lys Lys Thr Gly Gly Glu Lys Met Pro Val Gln Met Ile
1235 1240 1245

Gly Asp Ile Leu Ala Ala Glu Leu Ser His Met Gln Ala Tyr Ile
1250 1255 1260

Arg Phe Cys Ser Cys Gln Leu Asn Gly Ala Thr Leu Leu Gln Gln
1265 1270 1275

Lys Thr Asp Glu Asp Thr Asp Phe Lys Glu Phe Leu Lys Lys Leu
1280 1285 1290

Ala Ser Asp Pro Arg Cys Lys Gly Met Pro Leu Ser Ser Phe Leu
1295 1300 1305

Leu Lys Pro Met Gln Arg Ile Thr Arg Tyr Pro Leu Leu Ile Arg
1310 1315 1320

Ser Ile Leu Glu Asn Thr Pro Gln Ser His Val Asp His Ser Ser
1325 1330 1335

Leu Lys Leu Ala Leu Glu Arg Ala Glu Glu Leu Cys Ser Gln Val
1340 1345 1350

Asn Glu Gly Val Arg Glu Lys Glu Asn Ser Asp Arg Leu Glu Trp
1355 1360 1365

Ile Gln Ala His Val Gln Cys Glu Gly Leu Ala Glu Gln Leu Ile
1370 1375 1380

Phe Asn Ser Leu Thr Asn Cys Leu Gly Pro Arg Lys Leu Leu His
1385 1390 1395

Ser Gly Lys Leu Tyr Lys Thr Lys Ser Asn Lys Glu Leu His Ala
1400 1405 1410

Phe Leu Phe Asn Asp Phe Leu Leu Leu Thr Tyr Leu Val Arg Gln
1415 1420 1425

Phe Ala Ala Ala Ser Gly His Glu Lys Leu Phe Asn Ser Lys Ser
1430 1435 1440

Ser Ala Gln Phe Arg Met Tyr Lys Thr Pro Ile Phe Leu Asn Glu
1445 1450 1455

Val Leu Val Lys Leu Pro Thr Asp Pro Ser Gly Asp Glu Pro Val
1460 1465 1470

Phe His Ile Ser His Ile Asp Arg Val Tyr Thr Leu Arg Thr Asp
1475 1480 1485

Asn Ile Asn Glu Arg Thr Ala Trp Val Gln Lys Ile Lys Gly Ala
1490 1495 1500

Ser Glu Gln Tyr Ile Asp Thr Glu Lys Lys Lys Arg Glu Lys Ala
1505 1510 1515

Tyr Gln Ala Arg Ser Gln Lys Thr Ser Gly Ile Gly Arg Leu Met
1520 1525 1530

Val His Val Ile Glu Ala Thr Glu Leu Lys Ala Cys Lys Pro Asn
1535 1540 1545

Gly Lys Ser Asn Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser
1550 1555 1560

Tyr Thr Thr Arg Thr Leu Gln Asp Thr Leu Asn Pro Lys Trp Asn
1565 1570 1575

Phe Asn Cys Gln Phe Phe Ile Lys Asp Leu Tyr Gln Asp Val Leu

1580 1585 1590
Cys Leu Thr Met Phe Asp Arg Asp Gln Phe Ser Pro Asp Asp Phe
1595 1600 1605

Leu Gly Arg Thr Glu Val Pro Val Ala Lys Ile Arg Thr Glu Gln
1610 1615 1620

Glu Ser Lys Gly Pro Thr Thr Arg Arg Leu Leu Leu His Glu Val
1625 1630 1635

Pro Thr Gly Glu Val Trp Val Arg Phe Asp Leu Gln Leu Phe Glu
1640 1645 1650

Gln Lys Thr Leu Leu
1655

<210> 28
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 28
gaaggagaac tcagaccggc tggagtggat

30

<210> 29
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 29
gacagaggag cggtagatgg a

21

<210> 30
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 30
agctcccttg gttctggctt c

21

<210> 31
<211> 51

```

<212>  DNA
<213>  Artificial

<220>
<223>  Primer

<400>  31
gaattcagaa ccatggaaca aaagcttatt tctgaagaag acttggggcc c      51

<210>  32
<211>  37
<212>  DNA
<213>  Artificial

<220>
<223>  Primer

<400>  32
cctggattac aaggatgatg atgacaaatg actcgag      37

<210>  33
<211>  21
<212>  PRT
<213>  Artificial

<220>
<223>  Description of Artificial Sequence: Peptide

<400>  33

Met Ala Gln Phe Pro Thr Pro Phe Gly Gly Ser Leu Asp Val Trp Ala
1           5           10           15

Ile Thr Val Glu Glu
20

<210>  34
<211>  1270
<212>  PRT
<213>  Xenopus laevis

<400>  34

Met Ala Gln Phe Gly Thr Pro Phe Gly Gly Asn Leu Asp Ile Trp Ala
1           5           10           15

Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe His Gly Leu
20           25           30

Lys Pro Thr Ala Gly Tyr Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
35           40           45

Leu Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
50           55           60

```

Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Leu Glu Phe Ser Ile
65 70 75 80

Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Pro Leu Pro Ser
85 90 95

Ile Leu Pro Ser Asn Met Leu Lys Gln Pro Val Ala Met Pro Ala Ala
100 105 110

Ala Val Ala Gly Phe Gly Met Ser Gly Ile Val Gly Ile Pro Pro Leu
115 120 125

Ala Ala Val Ala Pro Val Pro Met Pro Ser Ile Pro Val Val Gly Met
130 135 140

Ser Pro Pro Leu Val Ser Ser Val Pro Thr Val Pro Pro Leu Ser Asn
145 150 155 160

Gly Ala Pro Ala Val Ile Gln Ser His Pro Ala Phe Ala His Ser Ala
165 170 175

Thr Leu Pro Lys Ser Ser Ser Phe Gly Arg Ser Val Ala Gly Ser Gln
180 185 190

Ile Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Pro Ala Pro
195 200 205

Pro Leu Val Val Glu Trp Ala Val Pro Ser Ser Ser Arg Leu Lys Tyr
210 215 220

Arg Gln Leu Phe Asn Ser Gln Asp Lys Thr Met Ser Gly Asn Leu Thr
225 230 235 240

Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln Ser
245 250 255

Gln Leu Ala Thr Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly Lys
260 265 270

Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val Ala
275 280 285

Met Ser Gly Gln Pro Leu Pro Pro Ile Leu Pro Pro Glu Tyr Ile Pro
290 295 300

Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Leu Ser Ile Met Ser
305 310 315 320

Ser Val Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Glu Glu Glu
325 330 335

Pro Gln Asn Ala Asp Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Lys
340 345 350

Arg Glu Asn Phe Glu Arg Gly Asn Leu Glu Leu Glu Lys Arg Arg Gln
355 360 365

Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln Leu
370 375 380

Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Asp Gln Glu
385 390 395 400

Arg Lys Arg Gln Gln Asp Leu Glu Lys Gln Leu Glu Lys Gln Arg Glu
405 410 415

Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg
420 425 430

Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp Glu
435 440 445

Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Arg Glu Gln Glu
450 455 460

Asp Ile Val Val Leu Lys Ala Lys Lys Lys Thr Leu Glu Phe Glu Leu
465 470 475 480

Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln Asp
485 490 495

Ile Arg Cys Arg Leu Thr Thr Gln Arg His Glu Ile Glu Ser Thr Asn
500 505 510

Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln Gln
515 520 525

Leu Gln Glu Ser Gln Gln Leu Leu Gly Lys Met Ile Pro Glu Lys Gln
530 535 540

Ser Leu Ile Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His Arg
545 550 555 560

Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Thr Lys Glu Ile Gly
565 570 575

Arg Gln Gln Leu Arg Asp Gln Leu Asp Glu Val Glu Lys Glu Thr Arg
580 585 590

Ala Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu Leu
595 600 605

Arg Glu Leu Tyr Asn Lys Gln Gln Phe Gln Lys Gln Gln Asp Phe Glu
610 615 620

Thr Glu Lys Ile Lys Gln Lys Glu Leu Glu Arg Lys Thr Ser Glu Leu
625 630 635 640

Asp Lys Leu Lys Glu Glu Asp Lys Arg Arg Met Leu Glu Gln Asp Lys
645 650 655

Leu Trp Gln Asp Arg Val Lys Gln Glu Glu Arg Tyr Lys Phe Gln
660 665 670

Asp Glu Glu Lys Glu Lys Arg Glu Glu Ser Val Gln Lys Cys Glu Val
675 680 685

Glu Lys Lys Pro Glu Ile Gln Glu Lys Pro Asn Lys Pro Phe His Gln
690 695 700

Pro Pro Glu Pro Gly Lys Leu Gly Gly Gln Ile Pro Trp Met Asn Thr
705 710 715 720

Glu Lys Ala Pro Leu Thr Ile Asn Gln Gly Asp Val Lys Val Val Tyr
725 730 735

Tyr Arg Ala Leu Tyr Pro Phe Asp Ala Arg Ser His Asp Glu Ile Thr
740 745 750

Ile Glu Pro Gly Asp Ile Ile Met Val Asp Glu Ser Gln Thr Gly Glu
755 760 765

Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly Lys Thr Gly Trp Phe Pro
770 775 780

Ala Asn Tyr Ala Glu Arg Met Pro Glu Ser Glu Phe Pro Ser Thr Thr

785

790

795

800

Lys Pro Ala Ala Glu Thr Thr Ala Lys Pro Thr Val His Val Ala Pro
805 810 815

Ser Pro Val Ala Pro Ala Ala Phe Thr Asn Thr Ser Thr Asn Ser Asn
820 825 830

Asn Trp Ala Asp Phe Ser Ser Thr Trp Pro Thr Asn Asn Thr Asp Lys
835 840 845

Val Glu Ser Asp Asn Trp Asp Thr Trp Ala Ala Gln Pro Ser Leu Thr
850 855 860

Val Pro Ser Ala Gly Gln His Arg Gln Arg Ser Ala Phe Thr Pro Ala
865 870 875 880

Thr Val Thr Gly Ser Ser Pro Ser Pro Val Leu Gly Gln Gly Glu Lys
885 890 895

Val Glu Gly Leu Gln Ala Gln Ala Leu Tyr Pro Trp Arg Ala Lys Lys
900 905 910

Asp Asn His Leu Asn Phe Asn Lys Asn Asp Val Ile Thr Val Leu Glu
915 920 925

Gln Gln Asp Met Trp Trp Phe Gly Glu Val Gln Gly Gln Lys Gly Trp
930 935 940

Phe Pro Lys Ser Tyr Val Lys Leu Ile Ser Gly Pro Leu Arg Lys Ser
945 950 955 960

Thr Ser Ile Asp Ser Thr Ser Ser Glu Ser Pro Ala Ser Leu Lys Arg
965 970 975

Val Ser Ser Pro Ala Phe Lys Pro Ala Ile Gln Gly Glu Glu Tyr Ile
980 985 990

Ser Met Tyr Thr Tyr Glu Ser Asn Glu Gln Gly Asp Leu Thr Phe Gln
995 1000 1005

Gln Gly Asp Leu Ile Val Val Ile Lys Lys Asp Gly Asp Trp Trp
1010 1015 1020

Thr Gly Thr Val Gly Glu Lys Thr Gly Val Phe Pro Ser Asn Tyr
1025 1030 1035

Val Arg Pro Lys Asp Ser Glu Ala Ala Gly Ser Gly Gly Lys Thr
1040 1045 1050

Gly Ser Leu Gly Lys Lys Pro Glu Ile Ala Gln Val Ile Ala Ser
1055 1060 1065

Tyr Ala Ala Thr Ala Pro Glu Gln Leu Thr Leu Ala Pro Gly Gln
1070 1075 1080

Leu Ile Leu Ile Arg Lys Lys Asn Pro Gly Gly Trp Trp Glu Gly
1085 1090 1095

Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Ile Gly Trp Phe Pro
1100 1105 1110

Ala Asn Tyr Val Lys Leu Leu Ser Pro Gly Thr Asn Lys Ser Thr
1115 1120 1125

Pro Thr Glu Pro Pro Lys Pro Thr Ser Leu Pro Pro Thr Cys Gln
1130 1135 1140

Val Ile Gly Met Tyr Asp Tyr Ile Ala Gln Asn Asp Asp Glu Leu
1145 1150 1155

Ala Phe Ser Lys Gly Gln Val Ile Asn Val Leu Asn Lys Glu Asp
1160 1165 1170

Pro Asp Trp Trp Lys Gly Glu Leu Asn Gly His Val Gly Leu Phe
1175 1180 1185

Pro Ser Asn Tyr Val Lys Leu Thr Thr Asp Met Asp Pro Ser Gln
1190 1195 1200

Gln Phe Arg Leu Gly Val Lys Pro Ala Gly Gly Ile Pro Ala Thr
1205 1210 1215

Gly Asp Arg Pro Phe Ile Leu Phe Pro Phe Arg Asp Gly Pro Ser
1220 1225 1230

Leu Leu Pro Asn Ala Phe Gln Ala Pro Pro Leu Ser Val Val Met
1235 1240 1245

Ile Lys Phe Arg Cys Phe Thr Ala Pro Arg Phe Cys Pro Asp Met
1250 1255 1260

Asn Val Lys Tyr Ile Asn Ile
1265 1270

<210> 35
<211> 1094
<212> PRT
<213> Drosophila melanogaster

<400> 35

Met Asn Ser Ala Val Asp Ala Trp Ala Val Thr Pro Arg Glu Arg Leu
1 5 10 15

Lys Tyr Gln Glu Gln Phe Arg Ala Leu Gln Pro Gln Ala Gly Phe Val
20 25 30

Thr Gly Ala Gln Ala Lys Gly Phe Phe Leu Gln Ser Gln Leu Pro Pro
35 40 45

Leu Ile Leu Gly Gln Ile Trp Ala Leu Ala Asp Thr Asp Ser Asp Gly
50 55 60

Lys Met Asn Ile Asn Glu Phe Ser Ile Ala Cys Lys Leu Ile Asn Leu
65 70 75 80

Lys Leu Arg Gly Met Asp Val Pro Lys Val Leu Pro Pro Ser Leu Leu
85 90 95

Ser Ser Leu Thr Gly Asp Val Pro Ser Met Thr Pro Arg Gly Ser Thr
100 105 110

Ser Ser Leu Ser Pro Leu Asp Pro Leu Lys Gly Ile Val Pro Ala Val
115 120 125

Ala Pro Val Val Pro Val Val Ala Pro Pro Val Ala Val Ala Thr Val
130 135 140

Ile Ser Pro Pro Gly Val Ser Val Pro Ser Gly Pro Thr Pro Pro Thr
145 150 155 160

Ser Asn Pro Pro Ser Arg His Thr Ser Ile Ser Glu Arg Ala Pro Ser
165 170 175

Ile Glu Ser Val Asn Gln Gly Glu Trp Ala Val Gln Ala Ala Gln Lys
180 185 190

Arg Lys Tyr Thr Gln Val Phe Asn Ala Asn Asp Arg Thr Arg Ser Gly

195

200

205

Tyr Leu Thr Gly Ser Gln Ala Arg Gly Val Leu Val Gln Ser Lys Leu
 210 215 220

Pro Gln Val Thr Leu Ala Gln Ile Trp Thr Leu Ser Asp Ile Asp Gly
 225 230 235 240

Asp Gly Arg Leu Asn Cys Asp Glu Phe Ile Leu Ala Met Phe Leu Cys
 245 250 255

Glu Lys Ala Met Ala Gly Glu Lys Ile Pro Val Thr Leu Pro Gln Glu
 260 265 270

Trp Val Pro Pro Asn Leu Arg Lys Ile Lys Ser Arg Pro Gly Ser Val
 275 280 285

Ser Gly Val Val Ser Arg Pro Gly Ser Gln Pro Ala Ser Arg His Ala
 290 295 300

Ser Val Ser Ser Gln Ser Gly Val Gly Val Val Asp Ala Asp Pro Thr
 305 310 315 320

Ala Gly Leu Pro Gly Gln Thr Ser Phe Glu Asp Lys Arg Lys Glu Asn
 325 330 335

Tyr Val Lys Gly Gln Ala Glu Leu Asp Arg Arg Arg Lys Ile Met Glu
 340 345 350

Asp Gln Gln Arg Lys Glu Arg Glu Glu Arg Glu Arg Lys Glu Arg Glu
 355 360 365

Glu Ala Asp Lys Arg Glu Lys Ala Arg Leu Glu Ala Glu Arg Lys Gln
 370 375 380

Gln Glu Glu Leu Glu Arg Gln Leu Gln Arg Gln Arg Glu Ile Glu Met
 385 390 395 400

Glu Lys Glu Glu Gln Arg Lys Arg Glu Leu Glu Ala Lys Glu Ala Ala
 405 410 415

Arg Lys Glu Leu Glu Lys Gln Arg Gln Gln Glu Trp Glu Gln Ala Arg
 420 425 430

Ile Ala Glu Met Asn Ala Gln Lys Glu Arg Glu Gln Glu Arg Val Leu
 435 440 445

Lys Gln Lys Ala His Asn Thr Gln Leu Asn Val Glu Leu Ser Thr Leu
450 455 460

Asn Glu Lys Ile Lys Glu Leu Ser Gln Arg, Ile Cys Asp Thr Arg Ala
465 470 475 480

Gly Val Thr Asn Val Lys Thr Val Ile Asp Gly Met Arg Thr Gln Arg
485 490 495

Asp Thr Ser Met Ser Glu Met Ser Gln Leu Lys Ala Arg Ile Lys Glu
500 505 510

Gln Asn Ala Lys Leu Leu Gln Leu Thr Gln Glu Arg Ala Lys Trp Glu
515 520 525

Ala Lys Ser Lys Ala Ser Gly Ala Ala Leu Gly Gly Glu Asn Ala Gln
530 535 540

Gln Glu Gln Leu Asn Ala Ala Phe Ala His Lys Gln Leu Ile Ile Asn
545 550 555 560

Gln Ile Lys Asp Lys Val Glu Asn Ile Ser Lys Glu Ile Glu Ser Lys
565 570 575

Lys Glu Asp Ile Asn Thr Asn Asp Val Gln Met Ser Glu Leu Lys Ala
580 585 590

Glu Leu Ser Ala Leu Ile Thr Lys Cys Glu Asp Leu Tyr Lys Glu Tyr
595 600 605

Asp Val Gln Arg Thr Ser Val Leu Glu Leu Lys Tyr Asn Arg Lys Asn
610 615 620

Glu Thr Ser Val Ser Ser Ala Trp Asp Thr Gly Ser Ser Ser Ala Trp
625 630 635 640

Glu Glu Thr Gly Thr Thr Val Thr Asp Pro Tyr Ala Val Ala Ser Asn
645 650 655

Asp Ile Ser Ala Leu Ala Ala Pro Ala Val Asp Leu Gly Gly Pro Ala
660 665 670

Pro Glu Gly Phe Val Lys Tyr Gln Ala Val Tyr Glu Phe Asn Ala Arg
675 680 685

Asn Ala Glu Glu Ile Thr Phe Val Pro Gly Asp Ile Ile Leu Val Pro
690 695 700

Leu Glu Gln Asn Ala Glu Pro Gly Trp Leu Ala Gly Glu Ile Asn Gly
705 710 715 720

His Thr Gly Trp Phe Pro Glu Ser Tyr Val Glu Lys Leu Glu Val Gly
725 730 735

Glu Val Ala Pro Val Ala Ala Val Glu Ala Pro Val Asp Ala Gln Val
740 745 750

Ala Asp Thr Tyr Asn Asp Asn Ile Asn Thr Ser Ser Ile Pro Ala Ala
755 760 765

Ser Ala Asp Leu Thr Ala Ala Gly Asp Val Glu Tyr Tyr Ile Ala Ala
770 775 780

Tyr Pro Tyr Glu Ser Ala Glu Glu Gly Asp Leu Ser Phe Ser Ala Gly
785 790 795 800

Glu Met Val Met Val Ile Lys Lys Glu Gly Glu Trp Trp Thr Gly Thr
805 810 815

Ile Gly Ser Arg Thr Gly Met Phe Pro Ser Asn Tyr Val Gln Lys Ala
820 825 830

Asp Val Gly Thr Ala Ser Thr Ala Ala Ala Glu Pro Val Glu Ser Leu
835 840 845

Asp Gln Glu Thr Thr Leu Asn Gly Asn Ala Ala Tyr Thr Ala Ala Pro
850 855 860

Val Glu Ala Gln Glu Gln Val Tyr Gln Pro Leu Pro Val Gln Glu Pro
865 870 875 880

Ser Glu Gln Pro Ile Ser Ser Pro Gly Val Gly Ala Glu Glu Ala His
885 890 895

Glu Asp Leu Asp Thr Glu Val Ser Gln Ile Asn Thr Gln Ser Lys Thr
900 905 910

Gln Ser Ser Glu Pro Ala Glu Ser Tyr Ser Arg Pro Met Ser Arg Thr
915 920 925

Ser Ser Met Thr Pro Gly Met Arg Ala Lys Arg Ser Glu Ile Ala Gln
930 935 940

Val Ile Ala Pro Tyr Glu Ala Thr Ser Thr Glu Gln Leu Ser Leu Thr
945 950 955 960

Arg Gly Gln Leu Ile Met Ile Arg Lys Lys Thr Asp Ser Gly Trp Trp
965 970 975

Glu Gly Glu Leu Gln Ala Lys Gly Arg Arg Arg Gln Ile Gly Trp Phe
980 985 990

Pro Ala Thr Tyr Val Lys Val Leu Gln Gly Gly Arg Asn Ser Gly Arg
995 1000 1005

Asn Thr Pro Val Ser Gly Ser Arg Ile Glu Met Thr Glu Gln Ile
1010 1015 1020

Leu Asp Lys Val Ile Ala Leu Tyr Pro Tyr Lys Ala Gln Asn Asp
1025 1030 1035

Asp Glu Leu Ser Phe Asp Lys Asp Asp Ile Ile Ser Val Leu Gly
1040 1045 1050

Arg Asp Glu Pro Glu Trp Trp Arg Gly Glu Leu Asn Gly Leu Ser
1055 1060 1065

Gly Leu Phe Pro Ser Asn Tyr Val Gly Pro Phe Val Thr Ser Gly
1070 1075 1080

Lys Pro Ala Lys Ala Asn Gly Thr Thr Lys Lys
1085 1090

<210> 36
<211> 12
<212> DNA
<213> Artificial

<220>
<223> 5' UTR

<400> 36
ggatccacca tg

12

<210> 37
<211> 12
<212> DNA
<213> Artificial

<220>
<223> Portion of cloning linker sequence

<400> 37
aagcttgggc cc

12